



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 140715

TO: Nita M Minnifield
Location: REM-3C01/3C18
Art Unit: 1645
Wednesday, December 22, 2004
Case Serial Number: 109/337584

From: Paul Schulwitz
Location: Biotech-Chem Library
REM-1A65
Phone: (571)272-2527

paul.schulwitz@uspto.gov

Search Notes

Examiner Minnifield,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Paul Schulwitz
Technical Information Specialist
STIC Biotech/Chem Library
(571)272-2527

*Reviewed
12/30/04
mm*

140715

From: Chan, Christina
Sent: Sunday, December 19, 2004 1:40 PM
To: Minnifield, Nita; STIC-Biotech/ChemLib
Subject: RE: rush sequence search

Importance: High

Please rush. Thanks Chris

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644
(571)-272-0841
Remsen, 3E89

-----Original Message-----

From: Minnifield, Nita
Sent: Sunday, December 19, 2004 1:39 PM
To: Chan, Christina
Subject: rush sequence search

Christina, please approve, 2 month amdt. due

STIC

09/337584

Please do a commercial and inteference sequence search on
SEQ ID NO: 3, 7, 10, 12, 38 and 57 of this application.

Please provide a paper copy of all results.

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2-_____
Date Searcher Picked up: _____
Date Completed: 12/22
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA Sequence: # _____
AA Sequence :# _____
Structure: # _____
Bibliographic: _____
Litigation: _____
Patent Family: _____
Other: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 21, 2004, 06:59:32 ; Search time 1539.25 Seconds
(without alignments)
614.453 Million cell updates/sec

Title: US-09-337-584-3

Perfect score: 20

Sequence: 1 tccataacgttcctgatgct 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_htg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	20	100.0	20	6	AR140486 Sequence
3	20	100.0	20	6	AR146337 Sequence
4	20	100.0	20	6	AR14674 Sequence
5	20	100.0	20	6	BD205559 Method of
6	20	100.0	20	6	BD261101 Methods a
7	20	100.0	20	6	BD261264 Methods a
8	20	100.0	20	6	BD267868 Methods f
9	20	100.0	20	6	BD270770 Stereoiso
10	20	100.0	20	6	AR213843 Sequence
11	20	100.0	20	6	AR222210 Sequence
12	20	100.0	20	6	AR352589 Sequence
13	20	100.0	20	6	AR432426 Sequence
14	20	100.0	20	6	AX104585 Sequence
15	20	100.0	20	6	AX105178 Sequence
16	20	100.0	20	6	AX351748 Sequence
17	20	100.0	20	6	AX351814 Sequence
18	20	100.0	20	6	AX351837 Sequence
19	20	100.0	20	6	AX351865 Sequence

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22	20	100.0	20	6	AX355517	AX355517 Sequence
23	20	100.0	20	6	AX455600	AX455600 Sequence
24	20	100.0	20	6	AX465343	AX465343 Sequence
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27	20	100.0	20	6	BD009051	BD009051 Immunost
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35	18.4	92.0	20	6	A90870	A90870 Sequence 5
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37	18.4	92.0	20	6	A93521	A93521 Sequence 14
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ALIGNMENTS

RESULT 1

AR140444

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1..20

/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

linear PAT 16-JUN-2001

20 bp DNA

Sequence 3 from patent US 6207646.

Unknown.

Unknown.

Unclassified.

1 (bases 1 to 20)

Krieg,A.M., Kline,J., Klinman,D. and Steinberg,A.D.

Immunostimulatory nucleic acid molecules

Patent: US 6207646-A 3 27-MAR-2001;

Location/Qualifiers

1..20

/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

linear PAT 16-JUN-2001

20 bp DNA

Sequence 45 from patent US 6207646.

Unknown.

Unclassified.

1 (bases 1 to 20)

Krieg,A.M., Kline,J., Klinman,D. and Steinberg,A.D.

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/mol_type="unassigned DNA"

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linear PAT 16-JUN-2001

20 bp DNA

Sequence 45 from patent US 6207646.

Unknown.

Unclassified.

1 (bases 1 to 20)

Krieg,A.M., Kline,J., Klinman,D. and Steinberg,A.D.

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OM nucleic - nucleic search, using sw model

Run on: December 21, 2004, 05:50:35 ; Search time 233.962 Seconds
(without alignments)
448.741 Million cell updates/sec

Title: US-09-337-584-3

Perfect score: 20

Sequence: 1 tccataacgttcctgatgct 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	2 AAV27642	AAV27642 Immunosti
2	20	100.0	20	2 AAV27670	AAV27670 Immunosti
3	20	100.0	20	2 AAV27709	AAV27709 Immunosti
4	20	100.0	20	2 AAV27652	AAV27652 Immunosti
5	20	100.0	20	2 AAV80113	AAV80113 Oligo use
6	20	100.0	20	2 AAZ41895	AZ41895 IL-12 sec
7	20	100.0	20	3 AAZ60967	AZ60967 Nucleotid
8	20	100.0	20	3 AAZ47971	AZ47971 Immune re
9	20	100.0	20	3 AAZ47842	AZ47842 Immunosti
10	20	100.0	20	3 AAZ47635	AZ47635 Parasitic
11	20	100.0	20	4 AAH50573	AAH50573 Mouse li-
12	20	100.0	20	4 AAH19253	AAH19253 Phosphodi
13	20	100.0	20	4 AAH19295	AAH19295 CpG Oligo
14	20	100.0	20	4 AAF98799	AAf98799 CpG immu
15	20	100.0	20	4 AAF99577	AAf99577 Immunosti
16	20	100.0	20	6 ABL35136	ABL35136 Immunosti
17	20	100.0	20	6 ABL35221	ABL35221 Immunosti
18	20	100.0	20	6 ABL35289	ABL35289 Immunosti
19	20	100.0	20	6 ABL35247	ABL35247 Immunosti
20	20	100.0	20	6 ABL35200	ABL35200 Immunosti
21	20	100.0	20	6 ABL35266	ABL35266 Immunosti

ALIGNMENTS

22	20	100.0	20	6 ABS78293	ABs78293 Angiogene
23	20	100.0	20	6 ABL39123	ABl39123 Immunosti
24	20	100.0	20	6 ABK46421	ABk46421 Immunosti
25	20	100.0	20	6 AAL39202	AAI39202 Murine To
26	20	100.0	20	6 ABS70555	ABs70555 Dendritic
27	20	100.0	20	9 ACA92700	ACa92700 Immunosti
28	20	100.0	20	9 ACD91401	ACd91401 Immunosti
29	20	100.0	20	9 ACH03115	ACH03115 Immunosti
30	20	100.0	20	9 ADB37079	ADb37079 Immunosti
31	20	100.0	20	10 AAD60205	AAd60205 Oligonuc
32	20	100.0	20	10 ADF09184	ADf09184 Immunomod
33	20	100.0	20	10 ADG68105	ADg68105 Unmethyla
34	20	100.0	20	10 ACF36783	ACf36783 Immunosti
35	20	100.0	20	10 ABX76032	ABx76032 Immunosti
36	20	100.0	20	10 ACA58697	ACa58697 Gastric u
37	20	100.0	20	12 ADI01045	ADi01045 Immunosti
38	20	100.0	20	12 ADM99014	ADm99014 Immunosti
39	20	100.0	20	12 ADO04730	ADo04730 CpG oligo
40	20	100.0	20	12 ADQ07464	ADq07464 Immunosti
41	20	100.0	24	6 ABL35310	ABl35310 Immunosti
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RESULT 1

AAV27642
ID AAV27642 standard; DNA; 20 BP.

XX AC AAV27642;

XX 01-OCT-1998 (first entry)

DE Immunostimulatory oligodeoxyribonucleotide of the invention.

KW Immunostimulatory; oligodeoxyribonucleotide; ODN;
KW unmethylated CpG dinucleotide; activate; lymphocyte; immune response;
KW Th2; Th1; cytokine; treatment; prevention; asthma; autoimmune disease;
KW desensitisation therapy; artificial adjuvant; antibody generation; ss.

XX Synthetic.

XX WO9818810-A1.

XX 07-MAY-1998.

XX 30-OCT-1997; 97WO-US019791.

XX 30-OCT-1996; 96US-00738652.

XX (IOWA) UNIV IOWA RES FOUND.

XX Krieg AM, Kline JN;

XX WPI, 1998-272127/24.

XX New immunostimulatory nucleic acid molecules - which contain at least one unmethylated CpG dinucleotide, used for treating e.g. tumours, infections or autoimmune disease.

XX Claim 23; Page 82; 109pp; English.

XX AAV27641-751 represent immunostimulatory oligodeoxyribonucleotides (ODNs) of the invention. The ODNs contain at least one unmethylated CpG dinucleotide, and have the formula: 5' N1X1CGX2N2 3', where at least one nucleotide separates consecutive CpGs, X1 is adenine, guanine, or thymine, X2 is cytosine or thymine, N1 is any nucleotide and N1+N2 is 0-26 bases with the provision that N1 and N2 does not contain a CCG tetramer or more than one CCG or CCG trimer OR 5' NX1X2CGX3X4N 3', where at least

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OM nucleic - nucleic search, using sw model

Run on: December 21, 2004, 08:31:21 ; Search time 44.9057 Seconds
(without alignments)
316.570 Million cell updates/sec

Title: US-09-337-584-3

Perfect score: 20

Sequence: 1 tccataacgttcctgatgct 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

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- 2: /cgn2_6/prodata/1/ina/5B COMB.seq.*
- 3: /cgn2_6/prodata/1/ina/6A COMB.seq.*
- 4: /cgn2_6/prodata/1/ina/6B COMB.seq.*
- 5: /cgn2_6/prodata/1/ina/PCUTS COMB.seq.*
- 6: /cgn2_6/prodata/1/ina/backfiles1.seq.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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4	20	100.0	20	3	US-08-738-652-3
5	20	100.0	20	4	US-08-960-774-3
6	20	100.0	20	4	US-08-960-774-3
7	20	100.0	20	4	US-08-960-774-3
8	20	100.0	20	4	US-08-960-774-3
9	18.4	92.0	20	2	US-09-337-619-3
10	18.4	92.0	20	3	US-08-386-063-25
11	18.4	92.0	20	3	US-08-386-063-25
12	18.4	92.0	20	3	US-08-386-063-25
13	18.4	92.0	20	3	US-08-738-652-3
14	18.4	92.0	20	3	US-08-738-652-3
15	18.4	92.0	20	3	US-08-738-652-44
16	18.4	92.0	20	3	US-08-738-652-54
17	18.4	92.0	20	3	US-08-738-652-54
18	18.4	92.0	20	3	US-08-960-774-7
19	18.4	92.0	20	3	US-08-960-774-88
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35	16.8	84.0	20	3	US-08-738-652-46	Sequence 46, Appli
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37	16.8	84.0	20	3	US-08-738-652-53	Sequence 47, Appli
38	16.8	84.0	20	3	US-09-030-701-5	Sequence 5, Appli
39	16.8	84.0	20	3	US-09-286-098-45	Sequence 45, Appli
40	16.8	84.0	20	3	US-09-286-098-48	Sequence 48, Appli
41	16.8	84.0	20	3	US-09-286-098-50	Sequence 50, Appli
42	16.8	84.0	20	3	US-09-286-098-51	Sequence 51, Appli
43	16.8	84.0	20	3	US-09-286-098-56	Sequence 56, Appli
44	16.8	84.0	20	3	US-09-286-098-57	Sequence 57, Appli
45	16.8	84.0	20	3	US-08-960-774-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1

US-08-738-652-3
; Sequence 3, Application US/08738652B
; Patent No. 6207646
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
; FILE REFERENCE: C1039/7004 HCL
; CURRENT APPLICATION NUMBER: US/08/738,652B
; EARLIER FILING DATE: 1996-10-30
; EARLIER APPLICATION NUMBER: US 08/276,358
; EARLIER FILING DATE: 1994-07-15
; EARLIER APPLICATION NUMBER: US 08/386,063
; EARLIER FILING DATE: 1995-02-07
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-08-738-652-3

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATACAGTTCCTGATGCT 20
DB 1 TCATACAGTTCCTGATGCT 20

RESULT 2

US-08-738-652-45
; Sequence 45, Application US/08738652B
; Patent No. 6207646
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
; FILE REFERENCE: C1039/7004 HCL
; CURRENT APPLICATION NUMBER: US/08/738,652B
; EARLIER FILING DATE: 1996-10-30
; EARLIER APPLICATION NUMBER: US 08/276,358
; EARLIER FILING DATE: 1994-07-15
; EARLIER APPLICATION NUMBER: US 08/386,063
; EARLIER FILING DATE: 1995-02-07
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 45

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OM nucleic - nucleic search, using sw model

Run on: December 21, 2004, 13:14:11 ; Search time 203.019 Seconds
(without alignments)
543.874 Million cell updates/sec

Title: US-09-337-584-3

Perfect score: 20

Sequence: 1 tcataacggtctctgatgct 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4093002 seqs, 276041825 residues

Total number of hits satisfying chosen parameters: 8186004

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 20: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	9	US-09-824-468-49
2	20	100.0	20	9	US-09-800-266A-43
3	20	100.0	20	9	US-09-895-007A-43
4	20	100.0	20	9	US-09-920-313-43
5	20	100.0	20	10	US-09-888-326-545
6	20	100.0	20	10	US-09-818-918-3
7	20	100.0	20	10	US-09-818-918-45
8	20	100.0	20	10	US-09-931-583-42
9	20	100.0	20	10	US-09-776-479-777
10	20	100.0	20	10	US-09-954-987B-77
11	20	100.0	20	11	US-09-874-991C-44
12	20	100.0	20	11	US-09-874-991C-110

13	20	100.0	20	11	US-09-874-991C-133	Sequence 133, App
14	20	100.0	20	11	US-09-874-991C-161	Sequence 161, App
15	20	100.0	20	11	US-09-874-991C-182	Sequence 182, App
16	20	100.0	20	11	US-09-874-991C-207	Sequence 207, App
17	20	100.0	20	11	US-09-776-479-777	Sequence 777, App
18	20	100.0	20	13	US-10-023-909A-43	Sequence 43, Appl
19	20	100.0	20	14	US-10-112-653-750	Sequence 750, App
20	20	100.0	20	14	US-10-017-995-777	Sequence 777, App
21	20	100.0	20	14	US-10-300-247-43	Sequence 43, Appl
22	20	100.0	20	15	US-10-161-229-44	Sequence 44, Appl
23	20	100.0	20	15	US-10-187-264A-3	Sequence 3, Appl
24	20	100.0	20	15	US-10-265-072-78	Sequence 78, Appl
25	20	100.0	20	15	US-10-306-522-3	Sequence 3, Appl
26	20	100.0	20	15	US-10-314-578-777	Sequence 777, App
27	20	100.0	20	15	US-10-434-696-43	Sequence 43, Appl
28	20	100.0	20	16	US-10-373-381-36	Sequence 36, Appl
29	20	100.0	20	16	US-10-719-493-3	Sequence 3, Appl
30	20	100.0	20	17	US-10-627-331-3	Sequence 3, Appl
31	20	100.0	20	17	US-10-666-733-43	Sequence 43, Appl
32	20	100.0	20	17	US-10-743-625-3	Sequence 3, Appl
33	20	100.0	20	17	US-10-743-625-45	Sequence 45, Appl
34	20	100.0	20	17	US-10-769-282-3	Sequence 3, Appl
35	20	100.0	20	17	US-10-769-282-45	Sequence 45, Appl
36	20	100.0	20	18	US-10-817-165-3	Sequence 3, Appl
37	20	100.0	20	18	US-10-817-165-45	Sequence 45, Appl
38	20	100.0	20	18	US-10-877-407-33	Sequence 33, Appl
39	20	100.0	20	18	US-10-816-220-43	Sequence 43, Appl
40	20	100.0	20	18	US-10-831-778-777	Sequence 777, App
41	20	100.0	20	18	US-10-876-892-36	Sequence 36, Appl
42	20	100.0	20	18	US-10-876-965-36	Sequence 36, Appl
43	20	100.0	20	18	US-10-877-369-36	Sequence 36, Appl
44	20	100.0	20	24	US-09-874-991C-228	Sequence 228, App
45	20	100.0	26	11	US-09-874-991C-51	Sequence 51, Appl

ALIGNMENTS

RESULT 1
US-09-824-468-49
; Sequence 49, Application US/09824468
; Patent No. US20020064515A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Weiner, George
; TITLE OF INVENTION: Methods and Products for Stimulating the Immune System Using Immunotherapeutic Oligonucleotides and Cytokines
; TITLE OF INVENTION: Immune System
; FILE REFERENCE: C1039/7026/HCL
; CURRENT APPLICATION NUMBER: US/09/824,468
; PRIOR FILING DATE: 2001-04-02
; PRIOR FILING DATE: 1999-04-02
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 49
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-824-468-49

Query Match 100.0%; Score 20; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCATAACGTTCTCTGATGCT 20

Db 1 TCATAACGTTCTCTGATGCT 20

RESULT 2

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 21, 2004, 08:28:35 ; Search time 2653.4 Seconds
(without alignments)
274.665 Million cell updates/sec

Title: US-09-337-584-3

Perfect score: 20

Sequence: 1 tccataacgtctctgatgct 20

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18.4	92.0	287	2	BF713668
2	18.4	92.0	648	6	CB176176
3	17.4	87.0	425	9	BX001224
4	17.4	87.0	855	7	CF932497
5	17.4	87.0	922	9	CNS01020
6	17.4	85.0	253	2	BB385734
7	16.8	84.0	158	2	BE164373
8	16.8	84.0	175	2	BB600645
9	16.8	84.0	217	9	CL808914
10	16.8	84.0	263	4	BG993633
11	16.8	84.0	341	2	BF457455
12	16.8	84.0	356	5	BP013861
13	16.8	84.0	365	1	AV962971
14	16.8	84.0	396	2	AW379917
15	16.8	84.0	424	5	BY241143
16	16.8	84.0	429	1	AU288167
17	16.8	84.0	429	1	AU288168
18	16.8	84.0	452	8	AZ162948
19	16.8	84.0	467	1	AIO47174
20	16.8	84.0	472	1	AJ449482
21	16.8	84.0	496	1	AV675486
22	16.8	84.0	509	5	BW268112
23	16.8	84.0	510	8	AQ683537
24	16.8	84.0	511	8	BH394304

25	16.8	84.0	526	8	BH393114
26	16.8	84.0	545	1	AV989385
27	16.8	84.0	556	1	AV997839
28	16.8	84.0	556	4	BI540503
29	16.8	84.0	556	8	BH395140
30	16.8	84.0	585	1	AV997837
31	16.8	84.0	587	9	CG793447
32	16.8	84.0	591	1	AJ453167
33	16.8	84.0	594	1	AJ454344
34	16.8	84.0	598	1	AJ452440
35	16.8	84.0	598	9	CE030744
36	16.8	84.0	614	1	AJ447301
37	16.8	84.0	617	5	BW347030
38	16.8	84.0	631	5	BP184578
39	16.8	84.0	638	1	AI981577
40	16.8	84.0	646	4	BM485876
41	16.8	84.0	650	8	BH375955
42	16.8	84.0	657	8	BH404989
43	16.8	84.0	658	8	BH381954
44	16.8	84.0	666	7	CK834056
45	16.8	84.0	667	2	BB630476

ALIGNMENTS

RESULT 1
BF713668
LOCUS
DEFINITION
ESTPBL223 differential display RT-PCR clones Sus scrofa cDNA clone
BL223, mRNA sequence.
ACCESSION
BF713668
VERSION
BF713668.1
KEYWORDS
EST.
SOURCE
Sus scrofa (pig)
ORGANISM
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE
1 (bases 1 to 287)
Ponsukilli, S., Wimmers, K. and Schellander, K.
Identification of porcine liver ESTs by differential display RT-PCR
Unpublished (2001)
JOURNAL
Contact: Ponsukilli S
Institute of Animal Breeding Science
University of Bonn
Endenicher Allee 15, Bonn 53115, Germany
Seq primer: T7 Sp6
High quality sequence stop: 287
POLYA=No.

FEATURES
Location/Qualifiers
1..287
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="BL223"
/note="Organ: liver; CDNA fragments obtained from differential display RT-PCR banding patterns were cloned into pGEM"

ORIGIN

Query Match
Best Local Similarity 92.0%; Score 18.4; DB 2; Length 287;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCCTAACGTTCTCTGATGCT 20

DB 14 TCCATGACGTTCTCTGATGCT 33

RESULT 2

CB176176

LOCUS
CB176176 648 bp mRNA linear EST 31-JAN-2003

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 21, 2004, 06:59:32 ; Search time 1539.25 Seconds
(without alignments)
614.453 Million cell updates/sec

Title: US-09-337-584-7

Perfect score: 20

Sequence: 1 tccatgacgttccctgatgct 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_htg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	20	100.0	20	6	A89782	A89782 Sequence 4
2	20	100.0	20	6	A89783	A89783 Sequence 5
3	20	100.0	20	6	A90869	A90869 Sequence 4
4	20	100.0	20	6	A90870	A90870 Sequence 5
5	20	100.0	20	6	A93512	A93512 Sequence 5
6	20	100.0	20	6	A93521	A93521 Sequence 14
7	20	100.0	20	6	AR078394	AR078394 Sequence
8	20	100.0	20	6	AR096710	AR096710 Sequence
9	20	100.0	20	6	AR135054	AR135054 Sequence
10	20	100.0	20	6	AR140448	AR140448 Sequence
11	20	100.0	20	6	AR140476	AR140476 Sequence
12	20	100.0	20	6	AR140485	AR140485 Sequence
13	20	100.0	20	6	AR140495	AR140495 Sequence
14	20	100.0	20	6	AR146312	AR146312 Sequence
15	20	100.0	20	6	AR154678	AR154678 Sequence
16	20	100.0	20	6	BD190423	BD190423 Microemul
17	20	100.0	20	6	BD205534	BD205534 Method of
18	20	100.0	20	6	BD251271	BD251271 Enhanceme
19	20	100.0	20	6	BD261076	BD261076 Methods a

20	20	100.0	20	6	BD261240	Methods a
21	20	100.0	20	6	BD261564	Vaccine.
22	20	100.0	20	6	BD267846	Methods f
23	20	100.0	20	6	BD270746	Stereoiso
24	20	100.0	20	6	CQ788117	Sequence
25	20	100.0	20	6	CQ788203	Sequence
26	20	100.0	20	6	CQ798386	Sequence
27	20	100.0	20	6	CQ812848	Sequence
28	20	100.0	20	6	CQ815139	Sequence
29	20	100.0	20	6	CQ829543	Sequence
30	20	100.0	20	6	AR182896	Sequence
31	20	100.0	20	6	AR182907	Sequence
32	20	100.0	20	6	AR213827	Sequence
33	20	100.0	20	6	AR222199	Sequence
34	20	100.0	20	6	AR237032	Sequence
35	20	100.0	20	6	AR237039	Sequence
36	20	100.0	20	6	AR303122	Sequence
37	20	100.0	20	6	AR392168	Sequence
38	20	100.0	20	6	AR432430	Sequence
39	20	100.0	20	6	AX023425	Sequence
40	20	100.0	20	6	AX040172	Sequence
41	20	100.0	20	6	AX104566	Sequence
42	20	100.0	20	6	AX104614	Sequence
43	20	100.0	20	6	AX104673	Sequence
44	20	100.0	20	6	AX105185	Sequence
45	20	100.0	20	6	AX135638	Sequence

ALIGNMENTS

RESULT 1
LOCUS A89782 20 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 4 from Patent WO9832462.
ACCESSION A89782
VERSION A89782.1 GI:6738296
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Lipford,G.B. and Heeg,K.
TITLE PHARMACEUTICAL COMPOSITIONS COMPRISING A POLYNUCLEOTIDE AND
OPTIONALLY AN ANTIGEN ESPECIALLY FOR VACCINATION
JOURNAL Patent: WO 9832462-A 4 30-JUL-1998;
LIPFORD GRAYSON B (DE); HEEG KLAUS (DE)
FEATURES
source
1..20
/organism="unclassified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 TCCATGACGTTCCCTGATGCT 20
|||||
Db 1 TCCATGACGTTCCCTGATGCT 20

RESULT 2
LOCUS A89783 20 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 5 from Patent WO9832462.
ACCESSION A89783
VERSION A89783.1 GI:6738297
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.

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OM nucleic - nucleic search, using sw model.

Run on: December 21, 2004, 05:50:35 ; Search time 233.962 Seconds
(without alignments)
448.741 Million cell updates/sec

Title: US-09-337-584-7

Perfect score: 20

Sequence: 1 tccatgacgttctctgatgct 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_23Sep04:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	2	AAT88792
2	20	100.0	20	2	AAT88792 Synthetic
3	20	100.0	20	2	Aav45996 Immune ad
4	20	100.0	20	2	Aav45995 Immune ad
5	20	100.0	20	2	Aav27708 Immunost
6	20	100.0	20	2	Aav27700 Immunost
7	20	100.0	20	2	Aav27651 Immunost
8	20	100.0	20	2	Aav72500 Cpg motif
9	20	100.0	20	2	Aaz41879 IL-12 sec
10	20	100.0	20	2	Aaz28190 Chlamydia
11	20	100.0	20	3	Aaa71935 Murine Th
12	20	100.0	20	3	Aaa48598 Immunost
13	20	100.0	20	3	Aaz60951 Nucleotid
14	20	100.0	20	3	Aaz47955 Immunost
15	20	100.0	20	3	Aaa90453 Cpg adjuv
16	20	100.0	20	3	Aaz99648 Nucleotid
17	20	100.0	20	3	Aaz99173 Inflammat
18	20	100.0	20	3	Aaz48858 B-cell st
19	20	100.0	20	3	Aaz47621 Parasitic
20	20	100.0	20	3	Aac60281 Immunost
21	20	100.0	20	4	Aah20398 Cpg motif

22	20	100.0	20	4	AAH43344
23	20	100.0	20	4	AAH50577
24	20	100.0	20	4	AAH23751
25	20	100.0	20	4	AAH75852
26	20	100.0	20	4	AAH19285
27	20	100.0	20	4	AAH19294
28	20	100.0	20	4	AAH19304
29	20	100.0	20	4	AAH19257
30	20	100.0	20	4	AAH98806
31	20	100.0	20	4	AAH02985
32	20	100.0	20	4	AAH99604
33	20	100.0	20	4	AAH99558
34	20	100.0	20	4	AAH99660
35	20	100.0	20	4	AAH20438
36	20	100.0	20	4	AAH92365
37	20	100.0	20	4	AAH43897
38	20	100.0	20	6	ABL35203
39	20	100.0	20	6	ABL35120
40	20	100.0	20	6	ABL35184
41	20	100.0	20	6	ABL35269
42	20	100.0	20	6	ABL35500
43	20	100.0	20	6	ABL35226
44	20	100.0	20	6	ABL35483
45	20	100.0	20	6	ABL35250

ALIGNMENTS

RESULT 1

AAT88792
ID AAT88792 standard; DNA; 20 BP.

AC AAT88792;

DT 24-APR-1998 (first entry)

DE Synthetic phosphorothioate oligonucleotide used as an adjuvant.

XX Parvovirus; feline; canine; T cell epitope; VP1; VP2; vaccine; immunogen;
KW phosphorothioate; cat; dog; mink; adjuvant; ss.

OS Synthetic.

PN WO9740163-A1.

PD 30-OCT-1997.

PF 18-APR-1997; 97WO-EP001943.

PR 19-APR-1996; 96EP-00106217.

XX (COLP/) COLPAN M.

XX Colpan M, Schorr J, Baker HJ, Smith BF;

XX WPI; 1997-535847/49.

XX Vaccine containing nucleic acid expressing parvoviral epitope - particularly both B and T cell epitope(s), for immunisation of cats, dogs and mink against parvoviruses, also as a carrier for other antigens.

PS Claim 17; Page 23; 30pp; English.

XX This is a synthetic phosphorothioate oligonucleotide used as an adjuvant in an anti-parvovirus vaccine. This adjuvant is particularly a DNA, containing unmethylated Cpg motifs i.e. ISO. The ISO contains phosphorothioate linkages and is also a powerful immune activator. The anti-parvovirus vaccine contains nucleic acid encoding at least one parvovirus-specific vpi or vp2 T/B cell antigenic epitope plus a carrier. The anti-parvovirus vaccine are especially used to protect cats, dogs and mink, e.g. against feline panleukopenia virus, mink enteritis virus or gastroenteritis caused by canine parvovirus (CPV). The vaccine may also

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OM nucleic - nucleic search, using sw model

Run on: December 21, 2004, 08:31:21 ; Search time 44.9057 Seconds
(without alignments)
316.570 Million cell updates/sec

Title: US-09-337-584-7

Perfect score: 20

Sequence: 1 tccatgacgttcctgatgct 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/ptodata1/ina/5A COMB.seq:*
- 2: /cgn2_6/ptodata1/ina/5B COMB.seq:*
- 3: /cgn2_6/ptodata1/ina/6A COMB.seq:*
- 4: /cgn2_6/ptodata1/ina/6B COMB.seq:*
- 5: /cgn2_6/ptodata1/ina/PCTUS COMB.seq:*
- 6: /cgn2_6/ptodata1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	20	100.0	20	2	US-09-133-774-11
2	20	100.0	20	3	US-08-386-063-25
3	20	100.0	20	3	US-09-303-862-11
4	20	100.0	20	3	US-08-386-063-25
5	20	100.0	20	3	US-08-738-652-7
6	20	100.0	20	3	US-08-738-652-35
7	20	100.0	20	3	US-08-738-652-44
8	20	100.0	20	3	US-08-738-652-54
9	20	100.0	20	3	US-09-286-098-24
10	20	100.0	20	3	US-08-960-774-7
11	20	100.0	20	3	US-09-082-649B-68
12	20	100.0	20	3	US-09-082-649B-79
13	20	100.0	20	4	US-09-325-193A-19
14	20	100.0	20	4	US-09-191-170-24
15	20	100.0	20	4	US-09-171-425-5
16	20	100.0	20	4	US-09-171-425-14
17	20	100.0	20	4	US-09-690-921-5
18	20	100.0	20	4	US-09-791-500-7
19	20	100.0	20	4	US-09-337-619-7
20	20	100.0	29	4	US-08-848-229-2
21	20	100.0	29	4	US-09-022-965-2
22	18.4	92.0	20	3	US-08-738-652-3
23	18.4	92.0	20	3	US-08-738-652-9
24	18.4	92.0	20	3	US-08-738-652-40
25	18.4	92.0	20	3	US-08-738-652-43
26	18.4	92.0	20	3	US-08-738-652-45
27	18.4	92.0	20	3	US-08-738-652-46

28	18.4	92.0	20	3	US-08-738-652-53
29	18.4	92.0	20	3	US-09-030-701-5
30	18.4	92.0	20	3	US-09-286-098-45
31	18.4	92.0	20	3	US-09-286-098-48
32	18.4	92.0	20	3	US-09-286-098-49
33	18.4	92.0	20	3	US-09-286-098-50
34	18.4	92.0	20	3	US-09-286-098-56
35	18.4	92.0	20	3	US-09-286-098-57
36	18.4	92.0	20	3	US-08-960-774-3
37	18.4	92.0	20	3	US-08-960-774-9
38	18.4	92.0	20	3	US-08-960-774-35
39	18.4	92.0	20	3	US-08-960-774-38
40	18.4	92.0	20	3	US-08-960-774-39
41	18.4	92.0	20	3	US-08-960-774-87
42	18.4	92.0	20	3	US-08-960-774-89
43	18.4	92.0	20	3	US-09-082-649B-71
44	18.4	92.0	20	4	US-09-325-193A-38
45	18.4	92.0	20	4	US-09-325-193A-42

ALIGNMENTS

RESULT 1

US-09-133-774-11
; Sequence 11, Application US/09133774B
; Patent No. 5962636
; GENERAL INFORMATION:
; APPLICANT: Bachmaier, Kurt
; APPLICANT: Hessel, Andrew J.
; APPLICANT: Neu M.D., Nikolaus
; APPLICANT: Penninger, Josef M.
; TITLE OF INVENTION: No. 5962636el Peptides Capable of Modulating Inflammatory Heart
; TITLE OF INVENTION: Disease
; FILE REFERENCE: A-536
; CURRENT APPLICATION NUMBER: US/09/133,774B
; CURRENT FILING DATE: 1998-08-12
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia trachomatis
; FEATURE:
; OTHER INFORMATION: An oligonucleotide derived from the DNA encoding a
; OTHER INFORMATION: 60 kDa cysteine rich outer membrane protein from
; OTHER INFORMATION: Chlamydia trachomatis.
US-09-133-774-11

Query Match 100.0%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCATGACGTTCTCTGATGCT 20
Db 1 TCCATGACGTTCTCTGATGCT 20

RESULT 2

US-08-386-063-25
; Sequence 25, Application US/08386063
; Patent No. 6008200
; GENERAL INFORMATION:
; APPLICANT: Arthur M. Krieg, M.D.
; TITLE OF INVENTION: IMMUNOMODULATORY OLIGONUCLEOTIDES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, SUITE 510
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02109-1875

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OM nucleic - nucleic search, using sw model

Run on: December 21, 2004, 13:14:11 ; Search time 203.019 Seconds
(without alignments)
543.874 Million cell updates/sec

Title: US-09-337-584-7

Perfect score: 20

Sequence: 1 tccatgacgttcctgatgct 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4093002 seqs, 2760418825 residues

Total number of hits satisfying chosen parameters: 8186004

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:
9: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:
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19: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:
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21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	20	100.0	20	9	US-09-800-266A-19
4	20	100.0	20	9	US-09-846-091-4
5	20	100.0	20	9	US-09-895-007A-19
6	20	100.0	20	9	US-09-920-313-19
7	20	100.0	20	10	US-09-415-142-25
8	20	100.0	20	10	US-09-888-326-127
9	20	100.0	20	10	US-09-888-326-566
10	20	100.0	20	10	US-09-888-326-567
11	20	100.0	20	10	US-09-818-918-7
12	20	100.0	20	10	US-09-818-918-35

13	20	100.0	20	10	US-09-818-918-44	Sequence 44, Appl
14	20	100.0	20	10	US-09-818-918-54	Sequence 54, Appl
15	20	100.0	20	10	US-09-931-583-25	Sequence 25, Appl
16	20	100.0	20	10	US-09-931-583-48	Sequence 48, Appl
17	20	100.0	20	10	US-09-776-479-758	Sequence 758, App
18	20	100.0	20	10	US-09-776-479-806	Sequence 806, App
19	20	100.0	20	10	US-09-776-479-865	Sequence 865, App
20	20	100.0	20	10	US-09-954-987B-84	Sequence 84, Appl
21	20	100.0	20	10	US-09-954-987B-207	Sequence 207, App
22	20	100.0	20	10	US-09-967-464-7	Sequence 7, Appl
23	20	100.0	20	11	US-09-874-991C-27	Sequence 27, Appl
24	20	100.0	20	11	US-09-874-991C-93	Sequence 93, Appl
25	20	100.0	20	11	US-09-874-991C-114	Sequence 114, App
26	20	100.0	20	11	US-09-874-991C-138	Sequence 138, App
27	20	100.0	20	11	US-09-874-991C-165	Sequence 165, App
28	20	100.0	20	11	US-09-874-991C-186	Sequence 186, App
29	20	100.0	20	11	US-09-874-991C-406	Sequence 406, App
30	20	100.0	20	11	US-09-874-991C-425	Sequence 425, App
31	20	100.0	20	11	US-09-776-479-758	Sequence 758, App
32	20	100.0	20	11	US-09-776-479-806	Sequence 806, App
33	20	100.0	20	11	US-09-776-479-865	Sequence 865, App
34	20	100.0	20	11	US-09-965-101-68	Sequence 68, Appl
35	20	100.0	20	11	US-09-965-101-79	Sequence 79, Appl
36	20	100.0	20	13	US-10-023-909A-19	Sequence 19, Appl
37	20	100.0	20	13	US-10-205-150-7	Sequence 7, Appl
38	20	100.0	20	14	US-10-011-635A-1	Sequence 1, Appl
39	20	100.0	20	14	US-10-112-653-10	Sequence 10, Appl
40	20	100.0	20	14	US-10-112-653-11	Sequence 11, Appl
41	20	100.0	20	14	US-10-112-653-731	Sequence 731, App
42	20	100.0	20	14	US-10-112-653-779	Sequence 779, App
43	20	100.0	20	14	US-10-112-653-836	Sequence 836, App
44	20	100.0	20	14	US-10-017-995-758	Sequence 758, App
45	20	100.0	20	14	US-10-017-995-806	Sequence 806, App

ALIGNMENTS

RESULT 1

US-09-791-500-7
; Sequence 7, Application US/09791500
; Patent No. US20020042387A1
; GENERAL INFORMATION:
; APPLICANT: Raz, Eval
; APPLICANT: Rachmilewitz, Daniel
; TITLE OF INVENTION: Method for Treating Inflammatory Bowel
; FILE OF INVENTION: Disease and Other Forms of Gastrointestinal Inflammation.
; FILE REFERENCE: 6510-202US1
; CURRENT APPLICATION NUMBER: US/09/791,500
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic polynucleotide sequence
US-09-791-500-7

Query Match 100.0%; Score 20; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCATGACGTTCCCTGATGCT 20
|||||
Db 1 TCCATGACGTTCCCTGATGCT 20
|||||

RESULT 2
US-09-824-468-24
; Sequence 24, Application US/09824468
; Patent No. US20020064515A1

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OM nucleic - nucleic search, using sw model

Run on: December 21, 2004, 08:28:35 ; Search time 2653.4 Seconds
(without alignments)
274.665 Million cell updates/sec

Title: US-09-337-584-7

Perfect score: 20

Sequence: 1 tccatgacgttcctgatgct 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750.

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1.*
2: gb_est2.*
3: gb_est3.*
4: gb_est4.*
5: gb_est5.*
6: gb_est6.*
7: gb_est7.*
8: gb_est8.*
9: gb_est9.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	18.4	92.0	777	6	CB313548	AGENCOURT
4	18.4	92.0	809	6	CB567435	AGENCOURT
5	17.4	87.0	370	5	BY153791	BY153791
6	17.4	87.0	392	1	AI077366	BY87611.x
7	17.4	87.0	408	1	AI086210	AI086210
8	17.4	87.0	593	8	CC317873	TAM32-3K8
9	17.4	87.0	688	8	AZ364551	IM0110C22
10	17.4	87.0	882	6	CA493454	AGENCOURT
11	17	85.0	389	9	CG260054	CG260054
12	17	85.0	497	9	CL179555	104.388.1
13	17	85.0	546	2	AW065908	687002G08
14	17	85.0	557	6	CA158051	SCERZ2305
15	17	85.0	614	6	CA113844	SCG1B103
16	17	85.0	646	6	CA109803	SCUTR106
17	17	85.0	663	6	CA153904	SCVPR2203
18	17	85.0	668	6	CA264770	SCAGT304
19	17	85.0	683	6	CA182313	SCBGT311
20	17	85.0	794	9	CG334934	OGWFR04TH
21	17	85.0	842	9	CG319646	OGA234TH
22	17	85.0	864	9	CG318330	OGXBB66TH
23	17	85.0	915	9	CG318342	OGXBB66TH
24	17	85.0	1051	6	CF258131	74 Tricho

C 25	16.8	84.0	70	1	AA855652	VW70G01.r
C 26	16.8	84.0	97	1	AA082589	AA082589 RN2309.r
C 27	16.8	84.0	127	8	CC200395	CC200395 ZR091.Ba
C 28	16.8	84.0	170	7	CN699738	CN699738 E0425G03-
C 29	16.8	84.0	185	5	BY012830	BY012830 EY012830
C 30	16.8	84.0	203	2	BB600029	BB600029 BB600029
C 31	16.8	84.0	216	2	BB590993	BB590993 BB590993
C 32	16.8	84.0	217	9	CL808914	CL808914 OR_CBA002
C 33	16.8	84.0	227	2	BB597403	BB597403 BB597403
C 34	16.8	84.0	242	2	BB604665	BB604665 BB604665
C 35	16.8	84.0	243	2	BB599612	BB599612 BB599612
C 36	16.8	84.0	245	2	BB603788	BB603788 BB603788
C 37	16.8	84.0	255	5	BY095951	BY095951 BY095951
C 38	16.8	84.0	266	2	BB596258	BB596258 BB596258
C 39	16.8	84.0	271	2	BB570188	BB570188 BB570188
C 40	16.8	84.0	272	2	BF913557	BF913557 MR3-UT012
C 41	16.8	84.0	275	2	BB585846	BB585846 BB585846
C 42	16.8	84.0	276	2	BB569248	BB569248 BB569248
C 43	16.8	84.0	277	2	BB601536	BB601536 BB601536
C 44	16.8	84.0	296	2	BB601186	BB601186 BB601186
C 45	16.8	84.0	296	5	BY126554	BY126554 BY126554

ALIGNMENTS

RESULT 1
BF713668

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BF713668 287 bp mRNA linear EST 31-DEC-2001
ESTPBL223 differential display RT-PCR clones Sus scrofa cDNA clone
BL223, mRNA sequence.

ACCESSION BF713668

VERSION BF713668.1 GI:18002858

KEYWORDS EST.

SOURCE Sus scrofa (pig)

ORGANISM Sus scrofa

REFERENCE 1 (bases 1 to 287)

AUTHORS Ponsuksilli, S., Wimmers, K. and Schellander, K.

TITLE Identification of porcine liver ESTs by differential display RT-PCR

JOURNAL Unpublished (2001)

COMMENT Contact: Ponsuksilli S
Institute of Animal Breeding Science
University of Bonn
Endenicher Allee 15, Bonn 53115, Germany
Seq primer: T7 SP6
High quality sequence stop: 287
POLYA=No.

FEATURES

source

Location/Qualifiers

1..287

/organism="Sus scrofa"

/mol_type="mRNA"

/db_xref="taxon:9823"

/clone="BL223"

/note="Organ: liver; cDNA fragments obtained from differential display RT-PCR banding patterns were cloned into pGEM"

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 20; DB 2; Length 287;

Mismatches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTGATGCT 20

DB 14 TCCATGACGTTCTGATGCT 33

RESULT 2

CC110844/c

LOCUS

CC110844

758 bp DNA linear GSS 16-APR-2003

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OM nucleic - nucleic search, using sw model

Run on: December 21, 2004, 06:59:32 ; Search time 1539.25 Seconds
(without alignments)
614.453 Million cell updates/sec

Title: US-09-337-584-10
Perfect score: 20
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
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8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_ey.*
13: gb_un.*
14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	20	100.0	20	6 AR140451	Sequence
3	20	100.0	20	6 AR146388	Sequence
4	20	100.0	20	6 AR146393	Sequence
5	20	100.0	20	6 AR154681	Sequence
6	20	100.0	20	6 BD190417	Microemul
7	20	100.0	20	6 BD205610	Method of
8	20	100.0	20	6 BD205615	Method of
9	20	100.0	20	6 BD222610	Compositi
10	20	100.0	20	6 BD251265	Enhanceme
11	20	100.0	20	6 BD261152	Methods a
12	20	100.0	20	6 BD261157	Methods a
13	20	100.0	20	6 BD261307	Methods a
14	20	100.0	20	6 BD261311	Methods a
15	20	100.0	20	6 BD261560	Vaccine. a
16	20	100.0	20	6 BD267913	Methods f
17	20	100.0	20	6 BD270813	Stereoiso
18	20	100.0	20	6 BD270817	Stereoiso
19	20	100.0	20	6 CQ753470	Sequence

20	100.0	20	6	CQ753471	Sequence
21	20	100.0	20	6 CQ769069	Sequence
22	20	100.0	20	6 CQ774838	Sequence
23	20	100.0	20	6 CQ788113	Sequence
24	20	100.0	20	6 CQ788199	Sequence
25	20	100.0	20	6 CQ815135	Sequence
26	20	100.0	20	6 CQ829537	Sequence
27	20	100.0	20	6 CQ829540	Sequence
28	20	100.0	20	6 AR182879	Sequence
29	20	100.0	20	6 AR182884	Sequence
30	20	100.0	20	6 AR182886	Sequence
31	20	100.0	20	6 AR213886	Sequence
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33	20	100.0	20	6 AR222263	Sequence
34	20	100.0	20	6 AR303118	Sequence
35	20	100.0	20	6 AR309879	Sequence
36	20	100.0	20	6 AR316578	Sequence
37	20	100.0	20	6 AR432433	Sequence
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39	20	100.0	20	6 AX020947	Sequence
40	20	100.0	20	6 AX020953	Sequence
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44	20	100.0	20	6 AX063575	Sequence
45	20	100.0	20	6 AX063580	Sequence

ALIGNMENTS

RESULT 1
AR078395 LOCUS
DEFINITION Sequence 12 from patent US 5962636.
ACCESSION AR078395
VERSION AR078395.1 GI:10005141
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bachmaier, K., Hessel, A. John., Neu, N. and Penninger, J. Martin.
TITLE Peptides capable of modulating inflammatory heart disease
JOURNAL Patent: US 5962636-A 12 05-OCT-1999;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCATGACGTTCTCTGACGTT 20
Db 1 TCCATGACGTTCTCTGACGTT 20

RESULT 2

AR140451 LOCUS
DEFINITION Sequence 10 from patent US 6207646.
ACCESSION AR140451
VERSION AR140451.1 GI:14482947
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Krieg, A.M., Kline, J., Klinman, D. and Steinberg, A.D.
TITLE Immunostimulatory nucleic acid molecules

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OM nucleic - nucleic search, using sw model

Run on: December 21, 2004, 05:50:35 ; Search time 233.962 Seconds
(without alignments)
448.741 Million cell updates/sec

Title: US-09-337-584-10

Perfect score: 20

Sequence: 1 tccatgacgtcttcgacgtt 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	20	100.0	20	AAV7683	Unmethy
3	20	100.0	20	AAV27667	Immunost
4	20	100.0	20	AAZ41946	IL-12 sec
5	20	100.0	20	AAZ41949	IL-12 sec
6	20	100.0	20	AAZ78802	HPV fusio
7	20	100.0	20	AAZ31943	CpG adjuv
8	20	100.0	20	AAV74237	CpG-N mot
9	20	100.0	20	AAV74244	CpG-N mot
10	20	100.0	20	AAV74242	CpG-N mot
11	20	100.0	20	AAZ88536	Cytosine-
12	20	100.0	20	AAZ28191	Chlamydia
13	20	100.0	20	AAZ61012	Nucleotid
14	20	100.0	20	AAZ61010	Nucleotid
15	20	100.0	20	AAZ48035	Immune re
16	20	100.0	20	AAZ48022	Immune re
17	20	100.0	20	AAZ48022	Immune re
18	20	100.0	20	AAZ47885	Immunost
19	20	100.0	20	AAZ47887	Immunost
20	20	100.0	20	AAZ90447	CpG adjuv
21	20	100.0	20	AAZ99174	Inflammat
22	20	100.0	20	AAZ99004	CpG motif

22	20	100.0	20	AAZ47601	Murine im
23	20	100.0	20	AAZ60277	Immunost
24	20	100.0	20	AAZ64136	Immunost
25	20	100.0	20	AAZ20390	CpG motif
26	20	100.0	20	AAZ20392	CpG motif
27	20	100.0	20	AAH50580	CpG motif
28	20	100.0	20	AAH19260	CpG motif
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37	20	100.0	20	AAH19260	CpG motif
38	20	100.0	20	AAH19260	CpG motif
39	20	100.0	20	AAH19260	CpG motif
40	20	100.0	20	AAH19260	CpG motif
41	20	100.0	20	AAH19260	CpG motif
42	20	100.0	20	AAH19260	CpG motif
43	20	100.0	20	AAH19260	CpG motif
44	20	100.0	20	AAH19260	CpG motif
45	20	100.0	20	AAH19260	CpG motif

ALIGNMENTS

RESULT 1
AAV60950
ID AAV60950 standard; DNA; 20 BP.
XX
AC AAV60950;
XX
DT 14-DEC-1998 (first entry)
XX
DE Unmethylated cytosine-guanine dinucleotide containing oligonucleotide 1.
KW ss; unmethylated CpG dinucleotide; immune response; natural killer cell;
KW Th2 response; Th1 response; Th1 cytokine; hepatitis B.
OS Synthetic.
XX
PN WO9840100-A1.
XX
PD 17-SEP-1998.
XX
PF 10-MAR-1998; 98WO-US004703.
XX
PR 10-MAR-1997; 97US-0040376P.
XX
PA (OTTA-) OTTAWA CIVIC LOEB RES INST.
PA (QIAG-) QIAGEN GMBH.
XX (IOWA) UNIV IOWA RES FOUND.
PI Davis HL, Schorr J, Krieg AM;
XX WPI; 1998-520792/44.
DR WPI; 1998-520792/44.
XX
PT Use of oligonucleotides containing an unmethylated CpG dinucleotide -
PT useful as, e.g. adjuvant with antigen, or nucleic acid encoding antigen
PT for inducing immune response in subject.
XX
PS Claim 14; Page 35; 67pp; English.
XX
CC Oligonucleotides containing at least 1 unmethylated CpG dinucleotide
CC affect the immune response in a subject by activating natural killer
CC cells or redirecting a subject's immune response from a Th2 to a Th1
CC response by inducing monocytic and other cells to produce Th1 cytokines.
CC These nucleic acids containing at least 1 unmethylated CpG can be used as
CC an adjuvant, specifically to induce an immune response against an
CC antigenic protein, and are used particularly for virally mediated

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OM nucleic - nucleic search, using sw model

Run on: December 21, 2004, 08:31:21 ; Search time 44.9057 Seconds
(without alignments)
316.570 Million cell updates/sec

Title: US-09-337-584-10

Perfect score: 20
Sequence: 1 tccatgacgttctctgacgtt 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	20	100.0	20	3	US-09-303-862-12
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4	20	100.0	20	3	US-09-030-701-62
5	20	100.0	20	3	US-09-286-098-100
6	20	100.0	20	3	US-09-286-098-105
7	20	100.0	20	3	US-08-960-774-10
8	20	100.0	20	3	US-09-082-649B-51
9	20	100.0	20	3	US-09-082-649B-56
10	20	100.0	20	3	US-09-082-649B-58
11	20	100.0	20	4	US-09-325-193A-86
12	20	100.0	20	4	US-09-325-193A-90
13	20	100.0	20	4	US-09-191-170-97
14	20	100.0	20	4	US-09-690-921-1
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18	20	100.0	20	4	US-10-405-231A-42
19	20	100.0	20	4	US-10-238-607-42
20	20	100.0	20	4	US-09-984-365-42
21	20	100.0	20	4	US-09-565-906-1
22	20	100.0	20	4	US-09-257-188A-2
23	20	100.0	44	3	US-09-082-649B-12
24	20	100.0	44	3	US-09-082-649B-13
25	17	85.0	17	3	US-09-030-701-39
26	17	85.0	17	3	US-09-286-098-70
27	17	85.0	17	3	US-08-960-774-70

28	17	85.0	17	4	US-09-325-193A-60	Sequence 60, Appl
29	17	85.0	17	4	US-09-191-170-64	Sequence 64, Appl
30	17	85.0	17	4	US-09-337-619-70	Sequence 70, Appl
31	16.8	84.0	20	2	US-09-133-774-11	Sequence 11, Appl
32	16.8	84.0	20	3	US-08-386-063-25	Sequence 25, Appl
33	16.8	84.0	20	3	US-09-303-862-11	Sequence 11, Appl
34	16.8	84.0	20	3	US-08-386-063-25	Sequence 25, Appl
35	16.8	84.0	20	3	US-08-738-652-7	Sequence 7, Appl
36	16.8	84.0	20	3	US-08-738-652-35	Sequence 35, Appl
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41	16.8	84.0	20	3	US-09-286-098-73	Sequence 73, Appl
42	16.8	84.0	20	3	US-09-286-098-84	Sequence 84, Appl
43	16.8	84.0	20	3	US-08-960-774-7	Sequence 7, Appl
44	16.8	84.0	20	3	US-08-960-774-73	Sequence 73, Appl
45	16.8	84.0	20	3	US-09-082-649B-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1

US-09-133-774-12
; Sequence 12, Application US/09133774B

; Patent No. 5962636

; GENERAL INFORMATION:

; APPLICANT: Bachmaier, Kurt

; APPLICANT: Hessel, Andrew J.

; APPLICANT: Neu M.D., Nikolaus

; APPLICANT: Penninger, Josef M.

; TITLE OF INVENTION: No. 5962636el Peptides Capable of Modulating Inflammatory Heart

; TITLE OF INVENTION: Disease

; FILE REFERENCE: A-536

; CURRENT APPLICATION NUMBER: US/09/133,774B

; CURRENT FILING DATE: 1998-08-12

; NUMBER OF SEQ ID NOS: 26

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 12

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Chlamydia trachomatis

; FEATURE:

; OTHER INFORMATION: An oligonucleotide derived from the DNA encoding a

; OTHER INFORMATION: 60 kDa cysteine rich outer membrane protein from

; OTHER INFORMATION: Chlamydia trachomatis.

US-09-133-774-12

Query Match 100.0%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 TCCATGACGTTCTCTGACGTT 20

RESULT 2

US-09-303-862-12

; Sequence 12, Application US/09303862

; Patent No. 6034230

; GENERAL INFORMATION:

; APPLICANT: Bachmaier, Kurt

; APPLICANT: Hessel, Andrew J.

; APPLICANT: Neu M.D., Nikolaus

; APPLICANT: Penninger, Josef M.

; TITLE OF INVENTION: No. 6034230el Peptides Capable of Modulating Inflammatory Heart

; FILE REFERENCE: A-536

; CURRENT APPLICATION NUMBER: US/09/303,862

; CURRENT FILING DATE: 1999-05-03

; EARLIER APPLICATION NUMBER: 09/133,774

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Run on: December 21, 2004, 13:14:11 / Search time 203.019 Seconds
(without alignments)
543.874 Million cell updates/sec

Title: US-09-337-584-10

Perfect score: 20

Sequence: 1 tccatgacgttcctgacgtt 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4093002 seqs, 2760418825 residues

Total number of hits satisfying chosen parameters: 8186004

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	20	100.0	20	9	US-09-917-222-1
7	20	100.0	20	9	US-09-800-266A-86
8	20	100.0	20	9	US-09-800-266A-90
9	20	100.0	20	9	US-09-895-007A-86
10	20	100.0	20	9	US-09-895-007A-90
11	20	100.0	20	9	US-09-920-313-86
12	20	100.0	20	9	US-09-920-313-90

13	20	100.0	20	10	US-09-888-326-560	Sequence 560, App
14	20	100.0	20	10	US-09-888-326-561	Sequence 561, App
15	20	100.0	20	10	US-09-888-326-562	Sequence 562, App
16	20	100.0	20	10	US-09-888-326-563	Sequence 563, App
17	20	100.0	20	10	US-09-818-918-10	Sequence 10, Appl
18	20	100.0	20	10	US-09-931-583-47	Sequence 69, Appl
19	20	100.0	20	10	US-09-776-479-69	Sequence 47, Appl
20	20	100.0	20	10	US-09-776-479-117	Sequence 137, App
21	20	100.0	20	10	US-09-776-479-152	Sequence 152, App
22	20	100.0	20	10	US-09-776-479-153	Sequence 153, App
23	20	100.0	20	10	US-09-776-479-223	Sequence 223, App
24	20	100.0	20	10	US-09-776-479-302	Sequence 302, App
25	20	100.0	20	10	US-09-776-479-948	Sequence 948, App
26	20	100.0	20	10	US-09-776-479-949	Sequence 949, App
27	20	100.0	20	10	US-09-776-479-950	Sequence 950, App
28	20	100.0	20	10	US-09-776-479-951	Sequence 951, App
29	20	100.0	20	10	US-09-776-479-952	Sequence 952, App
30	20	100.0	20	10	US-09-776-479-953	Sequence 953, App
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36	20	100.0	20	10	US-09-776-479-1023	Sequence 1023, Ap
37	20	100.0	20	10	US-09-954-987B-83	Sequence 83, Appl
38	20	100.0	20	10	US-09-967-464-1	Sequence 1, Appli
39	20	100.0	20	10	US-09-984-365-42	Sequence 42, Appl
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; Sequence 3, Application US/09760506
; Publication No. US20010034330A1
; GENERAL INFORMATION:
; APPLICANT: Kensil, Charlotte
; TITLE OF INVENTION: Innate Immunity-Stimulating Compositions of CpG and
; FILE REFERENCE: 8449-153-999
; CURRENT APPLICATION NUMBER: US/09/760,506
; CURRENT FILING DATE: 2002-01-12
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/200,853
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/175,840
; PRIOR FILING DATE: 2000-01-13
; PRIOR APPLICATION NUMBER: 60/128,608
; PRIOR FILING DATE: 1999-04-08
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; PRIOR FILING DATE: 1998-08-10
; NUMBER OF SEQ ID NOS: 6
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Motif
US-09-760-506-3

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Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGACGTTCTCCTGACGTT 20
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OM nucleic - nucleic search, using sw model

Run on: December 21, 2004, 08:28:35 ; Search time 2653.4 Seconds
(without alignments)
274.665 Million cell updates/sec

Title: US-09-337-584-10
Perfect score: 20
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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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9: gb_gest2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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7	16.8	84.0	497	9	CL179555
8	16.8	84.0	516	2	BF156008
9	16.8	84.0	546	2	AW065908
10	16.8	84.0	557	6	CA1158051
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14	16.8	84.0	668	6	CA264770
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16	16.8	84.0	715	5	BU253412
17	16.8	84.0	758	8	CC110844
18	16.8	84.0	794	9	CG334934
19	16.8	84.0	797	9	CNS02N06
20	16.8	84.0	814	5	BU205165
21	16.8	84.0	821	9	CNS03G84
22	16.8	84.0	842	9	CG319646
23	16.8	84.0	864	9	CG318330
24	16.8	84.0	908	6	CD791886

25	16.8	84.0	915	9	CG318342
26	16.8	84.0	958	5	BQ882047
27	16.8	84.0	992	5	AGENCOURT
28	16.8	84.0	994	9	CNS0421L
29	16.8	84.0	1867	3	CR696760
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32	16.4	82.0	392	6	BY630307
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ALIGNMENTS

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SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
ORIGIN
Query Match
Best Local Similarity
Matches
QY
DB

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genomic survey sequence.
GI:32114489
Zea mays
Zea mays
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
ciade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 886)
White, J., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Unpublished (2002)
Other_GSSs: OGUBV23TV
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
Class: sheared ends.
Location/Qualifiers
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OM nucleic - nucleic search, using sw model

Run on: December 21, 2004, 06:59:32 ; Search time 1539.25 Seconds
(without alignments)
614.453 Million cell updates/sec

Title: US-09-337-584-12

Perfect score: 20

Sequence: 1 999gtcaacgttgagg999g 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: gb_in:*

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5: gb_ov:*

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7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_srs:*

12: gb_sy:*

13: gb_un:*

14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	6	ARI40453 Sequence
2	20	100.0	20	6	ARI154761 Sequence
3	20	100.0	20	6	BD190419 Microemul
4	20	100.0	20	6	BD251367 Enhanceme
5	20	100.0	20	6	ARI182880 Sequence
6	20	100.0	20	6	ARI182887 Sequence
7	20	100.0	20	6	AR222213 Sequence
8	20	100.0	20	6	AR432435 Sequence
9	20	100.0	20	6	AX063578 Sequence
10	20	100.0	20	6	AX088932 Sequence
11	20	100.0	20	6	AX104327 Sequence
12	20	100.0	20	6	AX104575 Sequence
13	20	100.0	20	6	AX104776 Sequence
14	20	100.0	20	6	AX104777 Sequence
15	20	100.0	20	6	AX105103 Sequence
16	20	100.0	20	6	AX105236 Sequence
17	20	100.0	20	6	AX135634 Sequence
18	20	100.0	20	6	AX194489 Sequence
19	20	100.0	20	6	AX355408 Sequence

20	20	100.0	20	6	AX355409 Sequence
21	20	100.0	20	6	AX465439 Sequence
22	20	100.0	20	6	AX468483 Sequence
23	20	100.0	20	6	AX547380 Sequence
24	20	100.0	20	6	AX547628 Sequence
25	20	100.0	20	6	AX547829 Sequence
26	20	100.0	20	6	AX547830 Sequence
27	20	100.0	20	6	BD009060 Immunosti
28	20	100.0	20	6	BD069974 Use of nu
29	20	100.0	21	6	AX104812 Sequence
30	20	100.0	21	6	AX105257 Sequence
31	20	100.0	21	6	AX547865 Sequence
32	20	100.0	24	6	AX104326 Sequence
33	20	100.0	24	6	AX547379 Sequence
34	19	95.0	19	6	CQ753472 Sequence
35	19	95.0	19	6	CQ753473 Sequence
36	19	95.0	19	6	AX194446 Sequence
37	19	95.0	19	6	AX465396 Sequence
38	19	95.0	19	6	AX771751 Sequence
39	19	95.0	19	6	AX771752 Sequence
40	18.4	92.0	20	6	AR096686 Sequence
41	18.4	92.0	20	6	ARI35030 Sequence
42	18.4	92.0	20	6	AX342378 Sequence
43	18.4	92.0	20	6	AX342405 Sequence
44	18.4	92.0	20	6	AX342438 Sequence
45	17.4	87.0	19	6	ARI46340 Sequence

ALIGNMENTS

RESULT 1
ARI40453
LOCUS ARI40453 20 bp DNA linear PAT 16-JUN-2001
DEFINITION Sequence 12 from patent US 6207646.
ACCESSION ARI40453
VERSION ARI40453.1 GI:14482949
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 20)
Krieg,A.M., Kline,J., Klinman,D. and Steinberg,A.D.
AUTHORS Immunostimulatory nucleic acid molecules
TITLE Patent: US 6207646-A 12 27-MAR-2001;
JOURNAL Location/Qualifiers
FEATURES
source
1..20
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGGTCAACGTTGAGGGGG 20
Db 1 GGGGTCAACGTTGAGGGGG 20

RESULT 2
ARI154761
LOCUS ARI154761 20 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 90 from patent US 6239116.
ACCESSION ARI154761
VERSION ARI154761.1 GI:15122814
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 20)
Krieg,A.M. and Kline,J.N.
AUTHORS Immunostimulatory nucleic acid molecules
TITLE

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OM nucleic - nucleic search, using sw model

Run on: December 21, 2004, 05:50:35 ; Search time 233.962 Seconds
(without alignments)
448.741 Million cell updates/sec

Title: US-09-337-584-12

Perfect score: 20

Sequence: 1 ggggtcaacgttgagggggg 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 4: Geneseqn2001as:*
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- 6: Geneseqn2002as:*
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- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	20	100.0	20	2	AAV27654
4	20	100.0	20	2	AAV74238
5	20	100.0	20	2	AAV74245
6	20	100.0	20	3	AAV90449
7	20	100.0	20	4	AAH20394
8	20	100.0	20	4	AAH50658
9	20	100.0	20	4	AAH19262
10	20	100.0	20	4	AAF98854
11	20	100.0	20	4	AAF98731
12	20	100.0	20	4	AAH80669
13	20	100.0	20	4	AAF59504
14	20	100.0	20	4	AAF99567
15	20	100.0	20	4	AAF99764
16	20	100.0	20	4	AAF99390
17	20	100.0	20	4	AAF99763
18	20	100.0	20	4	AAV92361
19	20	100.0	20	4	AAH09639
20	20	100.0	20	5	AAF27750 P. falcip
21	20	100.0	20	6	ABH78484

22	20	100.0	20	6	ABS78485	ABS78485 Angiogene
23	20	100.0	20	6	ABS78283	ABS78283 Angiogene
24	20	100.0	20	6	ABS78035	ABS78035 Angiogene
25	20	100.0	20	6	ABL39032	ABL39032 Immunosti
26	20	100.0	20	6	ABL39033	ABL39033 Immunosti
27	20	100.0	20	6	ABK46517	ABK46517 Immunosti
28	20	100.0	20	6	AAI44488	AAI44488 CpG motif
29	20	100.0	20	6	ABS70558	ABS70558 Dendritic
30	20	100.0	20	8	ACC48308	ACC48308 CpG oligo
31	20	100.0	20	8	ABZ80163	ABZ80163 Immunosti
32	20	100.0	20	9	ACC83113	ACC83113 D class C
33	20	100.0	20	9	ACD99810	ACD99810 Immunosti
34	20	100.0	20	9	ACH03105	ACH03105 Immunosti
35	20	100.0	20	9	ACH03288	ACH03288 Immunosti
36	20	100.0	20	9	ADB37069	ADB37069 Immunosti
37	20	100.0	20	9	ADB37266	ADB37266 Immunosti
38	20	100.0	20	9	ADB36892	ADB36892 Immunosti
39	20	100.0	20	9	ADB37265	ADB37265 Immunosti
40	20	100.0	20	10	AAH60208	AAH60208 Oligonuc
41	20	100.0	20	10	ADG68114	ADG68114 Unmethyla
42	20	100.0	20	12	ADI01054	ADI01054 Immunosti
43	20	100.0	20	12	ACA63219	ACA63219 Toll-like
44	20	100.0	20	12	ADM99023	ADM99023 Immunosti
45	20	100.0	20	12	ADO04739	ADO04739 CpG oligo

ALIGNMENTS

RESULT 1

AAT16894

ID AAT16894 standard; DNA; 20 BP.

XX AAT16894;

XX AAT16894;

DT 06-SEP-1996 (first entry)

DE Immunomodulatory oligonucleotide contg. unmethylated C-G dinucleotide.

XX Unmethylated; immunomodulator; B cell activation; vaccine;
KW response stimulation; autoimmune disease; infection; ss.

OS Synthetic.

PN WO9602555-A1.

XX 01-FEB-1996.

XX 07-FEB-1995; 95WO-US001570.

XX 15-JUL-1994; 94US-00276358.

XX (IOWA) UNIV IOWA STATE RES FOUND INC.

PI Krieg AM;

DR WPI; 1996-105847/11.

XX Immunomodulatory oligonucleotide(s) contg. an un-methylated CpG di-nucleotide - used for stimulating activity or when methylated for inhibitory activity.

PS Claim 5; Page 39; 45pp; English.

XX AAT16894-T16898 are immunomodulatory oligonucleotides contg. at least one unmethylated C-G dinucleotide. The oligonucleotides can be used to activate B cells and natural killer cells. They can be used for treating, preventing or ameliorating an immune system deficiency, e.g. a tumour, cancer or a viral, fungal, bacterial or parasitic infection. They are also useful in stimulating a subject's response to a vaccine.

XX Sequence 20 BP; 3 A; 2 C; 12 G; 3 T; 0 U; 0 Other;

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OM nucleic - nucleic search, using sw model

Run on: December 21, 2004, 08:31:21 ; Search time 44.9057 Seconds
(without alignments)
316.570 Million cell updates/sec

Title: US-09-337-584-12

Perfect score: 20

Sequence: 1 ggggtcaacgttgagg9999 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*

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- 2: /cgn2_6/prodata/1/ina/5B_COMB.seq:*
- 3: /cgn2_6/prodata/1/ina/6A_COMB.seq:*
- 4: /cgn2_6/prodata/1/ina/6B_COMB.seq:*
- 5: /cgn2_6/prodata/1/ina/PCTUS_COMB.seq:*
- 6: /cgn2_6/prodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	3	US-08-738-652-12
2	20	100.0	20	3	US-09-030-701-63
3	20	100.0	20	3	US-08-960-774-90
4	20	100.0	20	3	US-09-082-649B-52
5	20	100.0	20	3	US-09-082-649B-59
6	20	100.0	20	4	US-09-191-170-47
7	20	100.0	20	4	US-09-337-619-12
8	18.4	92.0	20	3	US-08-386-063-1
9	18.4	92.0	20	3	US-08-386-063-1
10	17.4	87.0	19	3	US-09-030-701-21
11	17.4	87.0	19	3	US-09-286-098-52
12	17.4	87.0	19	3	US-08-960-774-12
13	17.4	87.0	19	4	US-09-325-193A-46
14	16.8	84.0	20	4	US-09-786-532-2
15	16	80.0	1426	4	US-09-464-535-41
16	15.8	79.0	1674	4	US-09-482-273-78
17	15.8	79.0	2312	4	US-09-620-312D-921
18	15.8	79.0	2312	4	US-09-620-312D-921
19	15.2	76.0	20	3	US-08-386-063-27
20	15.2	76.0	20	3	US-08-386-063-27
21	15.2	76.0	379	4	US-09-270-767-2945
22	15.2	76.0	379	4	US-09-270-767-18227
23	15.2	76.0	409	4	US-09-513-999C-15817
24	15.2	76.0	504	4	US-09-470-191-18
25	15.2	76.0	634	1	US-08-451-947-1
26	15.2	76.0	634	2	US-08-424-826A-1
27	15.2	76.0	634	3	US-08-928-694-1
28	15.2	76.0	634	3	US-08-928-694-1
29	15.2	76.0	634	3	US-08-928-694-1
30	15.2	76.0	634	3	US-08-928-694-1
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33	15.2	76.0	634	3	US-08-928-694-1
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37	15.2	76.0	634	3	US-08-928-694-1
38	15.2	76.0	634	3	US-08-928-694-1
39	15.2	76.0	634	3	US-08-928-694-1
40	15.2	76.0	634	3	US-08-928-694-1
41	15.2	76.0	634	3	US-08-928-694-1
42	15.2	76.0	634	3	US-08-928-694-1
43	15.2	76.0	634	3	US-08-928-694-1
44	15.2	76.0	634	3	US-08-928-694-1
45	15.2	76.0	634	3	US-08-928-694-1

C 28	15.2	76.0	634	4	US-08-450-842-1	Sequence 1, Appli
C 29	15.2	76.0	634	4	US-08-451-390-1	Sequence 1, Appli
C 30	15.2	76.0	634	5	PCT-US91-06950-1	Sequence 1, Appli
C 31	15.2	76.0	813	4	US-09-602-787A-471	Sequence 471, App
C 32	15.2	76.0	831	4	US-09-540-236-799	Sequence 799, App
C 33	15.2	76.0	1404	1	US-07-796-106-22	Sequence 22, Appl
C 34	15.2	76.0	1533	4	US-09-657-013-21	Sequence 21, Appl
C 35	15.2	76.0	1652	4	US-09-657-013-26	Sequence 26, Appl
C 36	15.2	76.0	1669	4	US-09-657-013-20	Sequence 20, Appl
C 37	15.2	76.0	2351	4	US-09-657-013-23	Sequence 23, Appl
C 38	15.2	76.0	3220	2	US-08-225-488-1	Sequence 1, Appli
C 39	15.2	76.0	10091	4	US-09-657-013-24	Sequence 24, Appl
C 40	15.2	76.0	10182	4	US-09-657-013-25	Sequence 25, Appl
C 41	15.2	76.0	10182	4	US-09-657-013-27	Sequence 27, Appl
C 42	15.2	76.0	10182	4	US-09-657-013-28	Sequence 28, Appl
C 43	15.2	76.0	11703	3	US-09-101-886B-3	Sequence 3, Appli
C 44	15.2	76.0	94750	4	US-09-596-002-38	Sequence 38, Appl
C 45	15.2	76.0	4403765	3	US-09-103-840A-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-08-738-652-12
; Sequence 12, Application US/08738652B
; Patent No. 6207646
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
; FILE REFERENCE: C1039/7004 HCL
; CURRENT APPLICATION NUMBER: US/08/738,652B
; CURRENT FILING DATE: 1996-10-30
; EARLIER APPLICATION NUMBER: US 08/276,358
; EARLIER FILING DATE: 1994-07-15
; EARLIER APPLICATION NUMBER: US 08/386,063
; EARLIER FILING DATE: 1995-02-07
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-08-738-652-12

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.65;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTCAACGTTGAGGGGGG 20
|||||
DB 1 GGGGTCAACGTTGAGGGGGG 20

RESULT 2

US-09-030-701-63
; Sequence 63, Application US/09030701B
; Patent No. 6214806
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schwartz, David A.
; TITLE OF INVENTION: USE OF NUCLEIC ACIDS CONTAINING UNMETHYLATED CPG DINUCLEOTIDE IN THE TREATMENT OF LPS-ASSOCIATED DISORDERS
; FILE REFERENCE: C1039/7011
; CURRENT APPLICATION NUMBER: US/09/030,701B
; CURRENT FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/039,405
; PRIOR FILING DATE: 1997-02-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: FastSeq for Windows Version 3.0

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 21, 2004, 13:14:11 ; Search time 203.019 Seconds
(without alignments)
543.874 Million cell updates/sec

Title: US-09-337-584-12

Perfect score: 20

Sequence: 1 999gtcaacgttgag99999 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4093002 seqs, 276041825 residues

Total number of hits satisfying chosen parameters: 8186004

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	20	100.0	20	10	US-09-818-918-12		Sequence 12, Appl
4	20	100.0	20	10	US-09-776-479-519		Sequence 519, App
5	20	100.0	20	10	US-09-776-479-767		Sequence 767, App
6	20	100.0	20	10	US-09-776-479-968		Sequence 968, App
7	20	100.0	20	10	US-09-776-479-969		Sequence 969, App
8	20	100.0	20	10	US-09-967-464-3		Sequence 3, Appl
9	20	100.0	20	11	US-09-776-479-519		Sequence 519, App
10	20	100.0	20	11	US-09-776-479-767		Sequence 767, App
11	20	100.0	20	11	US-09-776-479-968		Sequence 968, App
12	20	100.0	20	11	US-09-776-479-969		Sequence 969, App

13	20	100.0	20	11	US-09-965-101-52	Sequence 52, Appl
14	20	100.0	20	11	US-09-965-101-59	Sequence 59, Appl
15	20	100.0	20	14	US-10-112-653-496	Sequence 496, App
16	20	100.0	20	14	US-10-112-653-740	Sequence 740, App
17	20	100.0	20	14	US-10-112-653-923	Sequence 923, App
18	20	100.0	20	14	US-10-017-995-519	Sequence 519, App
19	20	100.0	20	14	US-10-017-995-767	Sequence 767, App
20	20	100.0	20	14	US-10-017-995-968	Sequence 968, App
21	20	100.0	20	14	US-10-017-995-969	Sequence 969, App
22	20	100.0	20	15	US-10-161-229-47	Sequence 47, Appl
23	20	100.0	20	15	US-10-194-035-89	Sequence 89, Appl
24	20	100.0	20	15	US-10-224-523-35	Sequence 35, Appl
25	20	100.0	20	15	US-10-187-264A-12	Sequence 12, Appl
26	20	100.0	20	15	US-10-306-523-12	Sequence 12, Appl
27	20	100.0	20	15	US-10-314-578-519	Sequence 519, App
28	20	100.0	20	15	US-10-314-578-767	Sequence 767, App
29	20	100.0	20	15	US-10-314-578-968	Sequence 968, App
30	20	100.0	20	15	US-10-314-578-969	Sequence 969, App
31	20	100.0	20	16	US-10-455-247-3	Sequence 3, Appl
32	20	100.0	20	16	US-10-719-493-12	Sequence 12, Appl
33	20	100.0	20	17	US-10-627-331-12	Sequence 12, Appl
34	20	100.0	20	17	US-10-743-625-12	Sequence 12, Appl
35	20	100.0	20	17	US-10-769-282-12	Sequence 12, Appl
36	20	100.0	20	18	US-10-817-165-12	Sequence 12, Appl
37	20	100.0	20	18	US-10-877-407-30	Sequence 30, Appl
38	20	100.0	20	18	US-10-831-778-519	Sequence 519, App
39	20	100.0	20	18	US-10-831-778-767	Sequence 767, App
40	20	100.0	20	18	US-10-831-778-968	Sequence 968, App
41	20	100.0	20	18	US-10-831-778-969	Sequence 969, App
42	20	100.0	20	18	US-10-486-755-14	Sequence 14, Appl
43	20	100.0	21	10	US-09-776-479-1004	Sequence 1004, Ap
44	20	100.0	21	11	US-09-776-479-1004	Sequence 1004, Ap
45	20	100.0	21	14	US-10-112-653-957	Sequence 957, App

ALIGNMENTS

RESULT 1
US-09-888-326-436
; Sequence 436, Application US/09888326
; Publication No. US20030026801A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, George
; TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
; FILE OF INVENTION: Cell Lysis and Treating Cancer
; FILE REFERENCE: C1039/7052 (AWS)
; CURRENT APPLICATION NUMBER: US/09/888,326
; CURRENT FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/213,346
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 848
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 436
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
; NAME/KEY: misc feature
; LOCATION: (0)-(0)
; OTHER INFORMATION: chimeric phosphorothioate/phosphodiester backbone
; OTHER INFORMATION: with phosphorothioate at 5' and 3' ends
US-09-888-326-436

Query Match 100.0%; Score 20; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTCAACGTTGAGGGGG 20

DB 1 GGGGTCAACGTTGAGGGGG 20

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OM nucleic - nucleic search, using sw model

Run on: December 21, 2004, 08:28:35 ; Search time 2653.4 Seconds
(without alignments)
: 274.665 Million cell updates/sec

Title: US-09-337-584-12

Perfect score: 20

Sequence: 1 ggggtcaacgttgagggggg 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_est3:*

4: gb_est4:*

5: gb_est5:*

6: gb_est6:*

7: gb_est7:*

8: gb_est8:*

9: gb_est9:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17.4	87.0	260	2	BB584327
2	17.4	87.0	708	2	BB629098
3	17.4	87.0	737	4	BG747032
4	17.4	87.0	957	5	BU956037
5	17.4	87.0	1244	5	BE962736
6	17.4	87.0	787	5	BX386891
7	17.4	87.0	791	9	CC506640
8	17.4	87.0	1008	5	BX356727
9	16.8	84.0	196	6	CA452850
10	16.8	84.0	244	7	CN657439
11	16.8	84.0	382	5	BY084323
12	16.8	84.0	406	4	BM001652
13	16.8	84.0	414	5	BX678404
14	16.8	84.0	457	5	BY277221
15	16.8	84.0	468	6	CA577271
16	16.8	84.0	473	7	CO076646
17	16.8	84.0	486	7	CF484305
18	16.8	84.0	508	4	BM003672
19	16.8	84.0	516	7	CO076740
20	16.8	84.0	522	7	CK391782
21	16.8	84.0	532	1	AL830714
22	16.8	84.0	533	4	BG355722
23	16.8	84.0	558	5	BX253788
24	16.8	84.0	569	7	CF895871

C 25	16.8	84.0	594	7	CF897160
C 26	16.8	84.0	595	7	CF896689
C 27	16.8	84.0	607	5	BQ18485
C 28	16.8	84.0	669	6	CB663538
C 29	16.8	84.0	680	4	BI716183
C 30	16.8	84.0	690	6	BY758462
C 31	16.8	84.0	692	8	BZ714778
C 32	16.8	84.0	700	2	BF607967
C 33	16.8	84.0	755	8	AZ099791
C 34	16.8	84.0	763	9	CC927270
C 35	16.8	84.0	766	8	BZ714768
C 36	16.8	84.0	777	8	AQ742337
C 37	16.8	84.0	793	8	BZ829333
C 38	16.8	84.0	806	4	BG671384
C 39	16.8	84.0	830	5	BU960761
C 40	16.8	84.0	837	5	BU940725
C 41	16.8	84.0	841	6	CA315476
C 42	16.8	84.0	855	5	BQ887367
C 43	16.8	84.0	873	7	CO809524
C 44	16.8	84.0	876	5	BQ942170
C 45	16.8	84.0	877	6	CB943360

ALIGNMENTS

RESULT 1	BB584327	260 bp	linear	EST 30-NOV-2000
LOCUS	BB584327	RIKEN full-length enriched, adult male epididymis Mus		
DEFINITION	musculus cDNA clone 9230105E24 5', mRNA sequence.			
ACCESSION	BB584327			
VERSION	BB584327.1	GI:11480871		
KEYWORDS	EST.			
SOURCE	Mus musculus (house mouse)			
ORGANISM	Mus musculus			
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
AUTHORS	1 (bases 1 to 260)			
	Aizawa, K., Akahira, S., Akimura, T., Arai, A., Arakawa, T., Carninci, P., Hanagaki, T., Hayatsu, N., Hiraoka, T., Hirozane, T., Hodojima, Y., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kawai, J., Kojima, Y., Konno, H., Kusakabe, M., Matsuyama, T., Miyazaki, A., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Okazaki, Y., Okido, T., Owa, C., Sakai, C., Sakai, K., Sasaki, D., Sato, K., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Tanaka, T., Toyota, T., Watahiki, A., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshiki, A., Muramatsu, M. and Hayashizaki, Y.			
TITLE	RIKEN Mouse ESTs (Aizawa, K. et al. 2000)			
JOURNAL	Unpublished (2000)			
COMMENT	Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suenro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-res@gs.riken.jp, URL: http://genome.gsc.riken.jp/ Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Thermotabilization and thermoactivation of thermostable enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998) Itoh, M., Kitaura, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y. Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999) Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999) Please visit our web site (http://genome.rtc.riken.go.jp) for			

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OM nucleic - nucleic search, using sw model

Run on: December 21, 2004, 06:59:32 ; Search time 1539.25 Seconds
(without alignments)
614.453 Million cell updates/sec

Title: US-09-337-584-38

Perfect score: 20
Sequence: 1 tccatgcgttcctgatgct 20

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_pa.*

2: gb_hcg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	6	AR140484 Sequence
2	20	100.0	20	6	AR140494 Sequence
3	20	100.0	20	6	AR146336 Sequence
4	20	100.0	20	6	AR146344 Sequence
5	20	100.0	20	6	AR146345 Sequence
6	20	100.0	20	6	AR154709 Sequence
7	20	100.0	20	6	BD190422 Microemul
8	20	100.0	20	6	BD205558 Method of
9	20	100.0	20	6	BD205566 Method of
10	20	100.0	20	6	BD205567 Method of
11	20	100.0	20	6	BD251270 Enhanceme
12	20	100.0	20	6	BD261100 Methods a
13	20	100.0	20	6	BD261108 Methods a
14	20	100.0	20	6	BD261109 Methods a
15	20	100.0	20	6	BD261270 Methods a
16	20	100.0	20	6	BD267867 Methods a
17	20	100.0	20	6	BD267874 Methods f
18	20	100.0	20	6	BD270776 Stereoiso
19	20	100.0	20	6	AR182899 Sequence

20	20	100.0	20	6	AR213849	Sequence
21	20	100.0	20	6	AR222209	Sequence
22	20	100.0	20	6	AR222217	Sequence
23	20	100.0	20	6	AR432461	Sequence
24	20	100.0	20	6	AX045773	Sequence
25	20	100.0	20	6	AX045774	Sequence
26	20	100.0	20	6	AX103944	Sequence
27	20	100.0	20	6	AX104567	Sequence
28	20	100.0	20	6	AX135637	Sequence
29	20	100.0	20	6	AX351747	Sequence
30	20	100.0	20	6	AX351813	Sequence
31	20	100.0	20	6	AX351836	Sequence
32	20	100.0	20	6	AX351864	Sequence
33	20	100.0	20	6	AX351885	Sequence
34	20	100.0	20	6	AX351910	Sequence
35	20	100.0	20	6	AX352126	Sequence
36	20	100.0	20	6	AX352145	Sequence
37	20	100.0	20	6	AX355034	Sequence
38	20	100.0	20	6	AX355583	Sequence
39	20	100.0	20	6	AX455619	Sequence
40	20	100.0	20	6	AX465348	Sequence
41	20	100.0	20	6	AX468486	Sequence
42	20	100.0	20	6	AX546997	Sequence
43	20	100.0	20	6	AX547620	Sequence
44	20	100.0	20	6	AX786558	Sequence
45	20	100.0	20	6	BD009091	Immunosti

ALIGNMENTS

RESULT 1	AR140484	Sequence 43 from patent US 6207646.	20 bp	DNA	linear	PAT 16-JUN-2001
LOCUS	AR140484	Sequence 43 from patent US 6207646.				
DEFINITION	AR140484					
ACCESSION	AR140484					
VERSION	AR140484.1	GI:14482980				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 20)					
AUTHORS	Krieg,A.M., Kline,J., Klinman,D. and Steinberg,A.D.					
TITLE	Immunostimulatory nucleic acid molecules					
JOURNAL	Patent: US 6207646-A 43 27-MAR-2001;					
FEATURES	Location/Qualifiers					
source	1..20					
	/organism="unknown"					
	/mol_type="unassigned DNA"					

ORIGIN

Query Match	100.0%	Score 20;	DB 6;	Length 20;
Best Local Similarity	100.0%	Pred. No. 8.7;		
Matches	20;	Conservative	0;	Mismatches
			0;	Indels
				Gaps
				0;

QY	1	TCCATGTCGTTCCCTGATGCT	20
DB	1	TCCATGTCGTTCCCTGATGCT	20

RESULT 2

LOCUS	AR140494	Sequence 53 from patent US 6207646.	20 bp	DNA	linear	PAT 16-JUN-2001
DEFINITION	AR140494					
ACCESSION	AR140494					
VERSION	AR140494.1	GI:14482990				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 20)					
AUTHORS	Krieg,A.M., Kline,J., Klinman,D. and Steinberg,A.D.					
TITLE	Immunostimulatory nucleic acid molecules					

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OM nucleic - nucleic search, using sw model

Run on: December 21, 2004, 05:50:35 ; Search time 233.962 Seconds
(without alignments)
448.741 Million cell updates/sec

Title: US-09-337-584-38

Perfect score: 20

Sequence: 1 tccatgcgtctctgatgct 20

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: N Geneseq_23Sep04:*

1: Geneseqn1980s:.*
2: Geneseqn1990s:.*
3: Geneseqn2000s:.*
4: Geneseqn2001as:.*
5: Geneseqn2001bs:.*
6: Geneseqn2002as:.*
7: Geneseqn2002bs:.*
8: Geneseqn2003as:.*
9: Geneseqn2003bs:.*
10: Geneseqn2003cs:.*
11: Geneseqn2003ds:.*
12: Geneseqn2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	2 AAV60952	Unmethyla
2	20	100.0	20	2 AAV47688	Unmethyla
3	20	100.0	20	2 AAV27647	Immunosti
4	20	100.0	20	2 AAV27707	Immunosti
5	20	100.0	20	2 AAZ41894	IL-12 sec
6	20	100.0	20	2 AAZ41903	IL-12 sec
7	20	100.0	20	3 AAZ60973	Nucleotid
8	20	100.0	20	3 AAZ47979	Immune re
9	20	100.0	20	3 AAZ47978	Immune re
10	20	100.0	20	3 AAZ47970	Immune re
11	20	100.0	20	3 AAZ47848	Immunosti
12	20	100.0	20	3 AAZ90452	CpG adjuv
13	20	100.0	20	3 AAZ47641	Parasitic
14	20	100.0	20	3 AAZ47634	Parasitic
15	20	100.0	20	3 AAZ63585	Immune st
16	20	100.0	20	4 AAH20397	CpG motif
17	20	100.0	20	4 AAC87224	Immunosti
18	20	100.0	20	4 AAC87225	Methylate
19	20	100.0	20	4 AAH50608	CpG motif
20	20	100.0	20	4 AAH19303	Non CpG o
21	20	100.0	20	4 AAH19293	CpG Oligo

ALIGNMENTS

RESULT 1
AAV60952
ID AAV60952 standard; DNA; 20 BP.
XX
AC AAV60952;
XX
DT 14-DEC-1998 (first entry)
XX
DE
XX
KW ss: unmethylated CpG dinucleotide; immune response; natural killer cell;
KW Th2 response; Th1 response; Th1 cytokine; hepatitis B.
XX Synthetic.
OS
XX
PN WO9840100-A1.
XX
PD 17-SEP-1998.
XX
PF 10-MAR-1998; 98WO-US004703.
XX
PR 10-MAR-1997; 97US-0040376P.
XX
PA (OTTA-) OTTAWA CIVIC LOEB RES INST.
PA (QIAG-) QIAGEN GMBH.
PA (IOWA) UNIV IOWA RES FOUND.
PI Davis HL, Schorr J, Krieg AM;
XX WPI; 1998-520792/44.
XX
PT Use of oligonucleotides containing an unmethylated CpG dinucleotide -
PT useful as, e.g. adjuvant with antigen, or nucleic acid encoding antigen
PT for inducing immune response in subject.
XX
PS Disclosure; Page 12; 67pp; English.
XX
CC Oligonucleotides containing at least 1 unmethylated CpG dinucleotide
CC affect the immune response in a subject by activating natural killer
CC cells or redirecting a subject's immune response from a Th2 to a Th1
CC response by inducing monocytic and other cells to produce Th1 cytokines.
CC These nucleic acids containing at least 1 unmethylated CpG can be used as
CC an adjuvant, specifically to induce an immune response against an
CC antigenic protein, and are used particularly for virally mediated

Aaf99011 Immunosti
Aaf99559 Immunosti
Aa92364 CG motif
Ab135498 Immunosti
Ab135265 Immunosti
Ab135288 Immunosti
Ab135199 Immunosti
Ab135220 Immunosti
Ab135515 Immunosti
Ab135135 Immunosti
Ab135246 Immunosti
Ab577652 Angiogene
Ab578275 Angiogene
Ab138700 Immunosti
Ab139189 Immunosti
Abk46426 Immunosti
Aal44491 CpG motif
Aal39221 Murine To
Aas70562 Dendritic
Ab570554 Dendritic
Abx89850 Cancer me
Aca92706 Immunosti
Acd91416 Immunosti
Ach03097 Immunosti

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OM nucleic - nucleic search, using sw model

Run on: December 21, 2004, 08:31:21 ; Search time 44.9057 Seconds
(without alignments)
316.570 Million cell updates/sec

Title: US-09-337-584-38

Perfect score: 20
Sequence: 1 tccatgctgctctgatgct 20

Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA: *
1: /cgn2_6/prodata/1/ina/5A-COMB.seq: *
2: /cgn2_6/prodata/1/ina/5B-COMB.seq: *
3: /cgn2_6/prodata/1/ina/6A-COMB.seq: *
4: /cgn2_6/prodata/1/ina/6B-COMB.seq: *
5: /cgn2_6/prodata/1/ina/6C-COMB.seq: *
6: /cgn2_6/prodata/1/ina/6D-COMB.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	3	US-08-738-652-43
2	20	100.0	20	3	US-08-738-652-53
3	20	100.0	20	3	US-09-030-701-5
4	20	100.0	20	3	US-09-286-098-48
5	20	100.0	20	3	US-09-286-098-56
6	20	100.0	20	3	US-09-286-098-57
7	20	100.0	20	3	US-08-960-774-38
8	20	100.0	20	3	US-09-082-6498-71
9	20	100.0	20	4	US-09-325-193A-49
10	20	100.0	20	4	US-09-191-170-43
11	20	100.0	20	4	US-09-191-170-51
12	20	100.0	20	4	US-09-337-619-38
13	19	95.0	20	3	US-09-030-701-25
14	19	95.0	20	3	US-08-960-774-44
15	19	95.0	20	3	US-09-082-6498-72
16	19	95.0	20	4	US-09-337-619-44
17	18.4	92.0	20	1	US-08-436-714-7
18	18.4	92.0	20	1	US-08-442-705-7
19	18.4	92.0	20	1	US-08-332-829-7
20	18.4	92.0	20	2	US-09-133-774-11
21	18.4	92.0	20	3	US-08-386-063-21
22	18.4	92.0	20	3	US-08-386-063-25
23	18.4	92.0	20	3	US-09-303-862-11
24	18.4	92.0	20	3	US-08-386-063-21
25	18.4	92.0	20	3	US-08-386-063-25
26	18.4	92.0	20	3	US-08-738-652-7
27	18.4	92.0	20	3	US-08-738-652-31

28	18.4	92.0	20	3	US-08-738-652-33	Sequence 33, Appl
29	18.4	92.0	20	3	US-08-738-652-34	Sequence 34, Appl
30	18.4	92.0	20	3	US-08-738-652-35	Sequence 35, Appl
31	18.4	92.0	20	3	US-08-738-652-37	Sequence 37, Appl
32	18.4	92.0	20	3	US-08-738-652-41	Sequence 41, Appl
33	18.4	92.0	20	3	US-08-738-652-42	Sequence 42, Appl
34	18.4	92.0	20	3	US-08-738-652-44	Sequence 44, Appl
35	18.4	92.0	20	3	US-08-738-652-54	Sequence 54, Appl
36	18.4	92.0	20	3	US-09-030-701-4	Sequence 4, Appl
37	18.4	92.0	20	3	US-09-286-098-22	Sequence 22, Appl
38	18.4	92.0	20	3	US-09-286-098-23	Sequence 23, Appl
39	18.4	92.0	20	3	US-09-286-098-24	Sequence 24, Appl
40	18.4	92.0	20	3	US-09-286-098-42	Sequence 42, Appl
41	18.4	92.0	20	3	US-09-286-098-46	Sequence 46, Appl
42	18.4	92.0	20	3	US-09-286-098-47	Sequence 47, Appl
43	18.4	92.0	20	3	US-08-960-774-28	Sequence 28, Appl
44	18.4	92.0	20	3	US-08-960-774-28	Sequence 28, Appl
45	18.4	92.0	20	3	US-08-960-774-36	Sequence 36, Appl

ALIGNMENTS

RESULT 1

US-08-738-652-43
; Sequence 43, Application US/08738652B
; Patent No. 6207646
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
; FILE REFERENCE: C1039/7004 HCL
; CURRENT APPLICATION NUMBER: US/08/738,652B
; CURRENT FILING DATE: 1996-10-30
; EARLIER APPLICATION NUMBER: US 08/276,358
; EARLIER FILING DATE: 1994-07-15
; EARLIER APPLICATION NUMBER: US 08/386,063
; EARLIER FILING DATE: 1995-02-07
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 43
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-08-738-652-43

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGTCGTTCTCTGATGCT 20
|||
DB 1 TCCATGTCGTTCTCTGATGCT 20

RESULT 2

US-08-738-652-53
; Sequence 53, Application US/08738652B
; Patent No. 6207646
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
; FILE REFERENCE: C1039/7004 HCL
; CURRENT APPLICATION NUMBER: US/08/738,652B
; CURRENT FILING DATE: 1996-10-30
; EARLIER APPLICATION NUMBER: US 08/276,358
; EARLIER FILING DATE: 1994-07-15
; EARLIER APPLICATION NUMBER: US 08/386,063
; EARLIER FILING DATE: 1995-02-07
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 53

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 21, 2004, 13:14:11 ; Search time 203.019 Seconds
(without alignments)
543.874 Million cell updates/sec

Title: US-09-337-584-38

Perfect score: 20

Sequence: 1 tccatgtcgttcctgatgct 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4093002 seqs, 2760418825 residues

Total number of hits satisfying chosen parameters: 8186004

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Published Applications NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US05_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
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- 10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 20: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	9	US-09-824-468-48
2	20	100.0	20	9	US-09-824-468-56
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4	20	100.0	20	9	US-09-800-266A-49
5	20	100.0	20	9	US-09-895-007A-49
6	20	100.0	20	9	US-09-920-313-49
7	20	100.0	20	10	US-09-888-326-62
8	20	100.0	20	10	US-09-888-326-611
9	20	100.0	20	10	US-09-818-918-43
10	20	100.0	20	10	US-09-818-918-53
11	20	100.0	20	10	US-09-931-583-57
12	20	100.0	20	10	US-09-776-479-136

13	20	100.0	20	10	US-09-776-479-759	Sequence 759, App	
14	20	100.0	20	10	US-09-954-987B-96	Sequence 96, Appl	
15	20	100.0	20	10	US-09-967-464-6	Sequence 6, Appl	
16	20	100.0	20	11	US-09-874-991C-43	Sequence 43, Appl	
17	20	100.0	20	11	US-09-874-991C-109	Sequence 109, App	
18	20	100.0	20	11	US-09-874-991C-132	Sequence 132, App	
19	20	100.0	20	11	US-09-874-991C-160	Sequence 160, App	
20	20	100.0	20	11	US-09-874-991C-181	Sequence 181, App	
21	20	100.0	20	11	US-09-874-991C-206	Sequence 206, App	
22	20	100.0	20	11	US-09-874-991C-422	Sequence 422, App	
23	20	100.0	20	11	US-09-874-991C-441	Sequence 441, App	
c	24	20	100.0	20	11	US-09-776-479-136	Sequence 136, App
25	20	100.0	20	11	US-09-776-479-759	Sequence 759, App	
26	20	100.0	20	11	US-09-965-101-71	Sequence 71, Appl	
27	20	100.0	20	13	US-10-023-909A-49	Sequence 49, Appl	
28	20	100.0	20	13	US-10-074-956-2	Sequence 2, Appl	
29	20	100.0	20	14	US-10-112-653-8	Sequence 8, Appl	
c	30	20	100.0	20	14	US-10-112-653-129	Sequence 129, App
31	20	100.0	20	14	US-10-112-653-732	Sequence 732, App	
c	32	20	100.0	20	14	US-10-017-995-136	Sequence 136, App
33	20	100.0	20	14	US-10-017-995-759	Sequence 759, App	
34	20	100.0	20	14	US-10-300-247-49	Sequence 49, Appl	
35	20	100.0	20	15	US-10-161-229-43	Sequence 43, Appl	
c	36	20	100.0	20	15	US-10-187-264A-38	Sequence 38, Appl
37	20	100.0	20	15	US-10-265-072-94	Sequence 94, Appl	
38	20	100.0	20	15	US-10-306-523-38	Sequence 38, Appl	
c	39	20	100.0	20	15	US-10-314-578-136	Sequence 136, App
40	20	100.0	20	15	US-10-314-578-759	Sequence 759, App	
41	20	100.0	20	15	US-10-434-696-49	Sequence 49, Appl	
42	20	100.0	20	16	US-10-373-381-43	Sequence 43, Appl	
43	20	100.0	20	16	US-10-373-381-44	Sequence 44, Appl	
44	20	100.0	20	16	US-10-719-493-38	Sequence 38, Appl	
45	20	100.0	20	17	US-10-627-331-38	Sequence 38, Appl	

ALIGNMENTS

RESULT 1

US-09-824-468-48

; Sequence 48, Application US/09824468

; Patent No. US20020064515A1

; GENERAL INFORMATION:

; APPLICANT: Krieg, Arthur M.

; TITLE OF INVENTION: Methods and Products for Stimulating the

; TITLE OF INVENTION: Immune System Using Immunotherapeutic Oligonucleotides and

; FILE OF INVENTION: Cytokines

; FILE REFERENCE: C1039/7026/HCL

; CURRENT APPLICATION NUMBER: US/09/824,468

; CURRENT FILING DATE: 2001-04-02

; PRIOR APPLICATION NUMBER: 09/286,098

; PRIOR FILING DATE: 1999-04-02

; NUMBER OF SEQ ID NOS: 105

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 48

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic Sequence

US-09-824-468-48

Query Match 100.0%; Score 20; DB 9; Length 20;

Best Local Similarity 100.0%; Pred. No. 3.7;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCATGTCGTCCTCATGCT 20

Db 1 TCCATGTCGTCCTCATGCT 20

RESULT 2

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 21, 2004, 08:28:35 ; Search time 2653.4 Seconds
(without alignments)
274.665 Million cell updates/sec

Title: US-09-337-584-38

Perfect score: 20

Sequence: 1 tccatgtcgttcctgatgct 20

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST.*

1: gb_est1.*
2: gb_est2.*
3: gb_hic.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_gss1.*
9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
C 1	18.4	92.0	70	1	AA855652 vw70g01.r
C 2	18.4	92.0	97	1	AA082589 zn23g09.r
C 3	18.4	92.0	287	2	BF713668 ESTPBL223
C 4	18.4	92.0	435	5	BY253224 BY253224
C 5	18.4	92.0	461	8	AZ721917 RPCI-24-1
C 6	18.4	92.0	484	4	BI899835 ib66d01.y
C 7	18.4	92.0	490	5	BU572806 PA_Ea000
C 8	18.4	92.0	520	6	CA573700 K0604E04-
C 9	18.4	92.0	522	6	CA547142 K0143B06-
C 10	18.4	92.0	532	6	CA545112 K0108B06-
C 11	18.4	92.0	539	5	BU575237 PA_Ea000
C 12	18.4	92.0	556	8	AZ752416 RPCI-24-6
C 13	18.4	92.0	571	8	AZ023370 RPCI-23-3
C 14	18.4	92.0	575	5	BU574826 PA_Ea000
C 15	18.4	92.0	578	4	BM730295 ih6g03.y
C 16	18.4	92.0	585	5	BP767484 BP767484
C 17	18.4	92.0	592	8	AZ985535 2M0267K19
C 18	18.4	92.0	608	4	BI100477 602886587
C 19	18.4	92.0	630	4	BI330822 602981204
C 20	18.4	92.0	636	2	BB654216 BB654216
C 21	18.4	92.0	637	4	EG863609 602796816
C 22	18.4	92.0	638	4	BI329902 602980033
C 23	18.4	92.0	642	2	BP229738 602029243
C 24	18.4	92.0	646	2	BE368574 601220573

C 25	18.4	92.0	649	5	BP765421
C 26	18.4	92.0	669	2	BE290326
C 27	18.4	92.0	674	6	CF169634
C 28	18.4	92.0	679	8	AZ837234
C 29	18.4	92.0	684	4	BG862940
C 30	18.4	92.0	685	4	BG974078
C 31	18.4	92.0	689	5	BU613249
C 32	18.4	92.0	700	5	BM944939
C 33	18.4	92.0	702	7	CF739812
C 34	18.4	92.0	705	6	CA317115
C 35	18.4	92.0	713	6	CA319143
C 36	18.4	92.0	727	8	AZ915252
C 37	18.4	92.0	730	4	BI904426
C 38	18.4	92.0	731	6	CB950574
C 39	18.4	92.0	734	6	CB948065
C 40	18.4	92.0	735	6	CB948157
C 41	18.4	92.0	737	8	AZ901548
C 42	18.4	92.0	738	4	BG862224
C 43	18.4	92.0	741	8	BH057351
C 44	18.4	92.0	743	4	BI695125
C 45	18.4	92.0	746	4	BI147210

ALIGNMENTS

RESULT 1
AA855652/c

LOCUS
DEFINITION

AA855652 70 bp mRNA linear EST 06-MAR-1998
vw70g01.r1 Stratagene mouse heart (#937316) Mus musculus cDNA clone
IMAGE:1260336 5' similar to gb:M11301 Mouse (MOUSE);, mRNA
sequence.

ACCESSION
AA855652

VERSION
EST.

KEYWORDS
SOURCE

ORGANISM
Mus musculus (house mouse)

REFERENCE
AUTHORS

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 70)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisler, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schallenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info:image.lnl.gov) for further information.
MGI:662888

TITLE
JOURNAL

COMMENT

Seq primer: -28ml3 rev1 ET from Amersham
High quality sequence stop: 19.
Location/Qualifiers
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/strain="NIH Swiss"
/db_xref="taxon:10090"
/clone="IMAGE:1260336"
/sex="pooled"
/tissue_type="heart"
/dev_stages="13 day embryos"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="Stratagene mouse heart (#937316)"
/note="Organ: heart; Vector: pBluescript SK-; Site 1:
EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:

FEATURES
source

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 21, 2004, 06:59:32 ; Search time 461.774 Seconds
(without alignments)
614.453 Million cell updates/sec

Title: US-09-337-584-57

Perfect score: 6

Sequence: 1 gtcgtt 6

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0*

Maximum Match 100*

Listing first 45 summaries

Database :

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1: gb_ba.*
2: gb_htg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6	100.0	6	CQ801400	Sequence
2	6	100.0	6	AX104952	Sequence
3	6	100.0	6	AX455589	Sequence
4	6	100.0	6	AX465334	Sequence
5	6	100.0	6	BD069960	Use of nu
6	6	100.0	7	BD267915	Methods f
7	6	100.0	7	AX455643	Sequence
8	6	100.0	7	AX465336	Sequence
9	6	100.0	7	BD013729	Method of
10	6	100.0	7	BD069928	Use of nu
11	6	100.0	8	E40310	Polynucleot
12	6	100.0	8	E40311	Polynucleot
13	6	100.0	8	E40312	Polynucleot
14	6	100.0	8	AX104953	Sequence
15	6	100.0	8	AX114123	Sequence
16	6	100.0	8	BD013682	Method of
17	6	100.0	8	BD017097	Substrate
18	6	100.0	10	BD240666	Preparati
19	6	100.0	10	E64719	Method for

C 20	6	100.0	10	6	AR222986	Sequence
C 21	6	100.0	10	6	AR303697	Sequence
C 22	6	100.0	10	6	AR303705	Sequence
C 23	6	100.0	10	6	AX153052	Sequence
C 24	6	100.0	10	6	AX362616	Sequence
C 25	6	100.0	10	6	BD065105	Character
C 26	6	100.0	10	6	BD091161	PSJ-induc
C 27	6	100.0	11	6	BD174616	Modified
C 28	6	100.0	11	6	CQ776205	Sequence
C 29	6	100.0	11	6	CQ776221	Sequence
C 30	6	100.0	11	6	CQ776284	Sequence
C 31	6	100.0	11	6	CQ833423	Sequence
C 32	6	100.0	11	6	AX825408	Sequence
C 33	6	100.0	11	6	AX626514	Sequence
C 34	6	100.0	11	6	AX630376	Sequence
C 35	6	100.0	11	9	S83243	CF transmem
C 36	6	100.0	12	6	A30298	Synthetic I
C 37	6	100.0	12	6	A91493	Sequence 20
C 38	6	100.0	12	6	AR021360	Sequence
C 39	6	100.0	12	6	AR042922	Sequence
C 40	6	100.0	12	6	AR084615	Sequence
C 41	6	100.0	12	6	AR161214	Sequence
C 42	6	100.0	12	6	AR167667	Sequence
C 43	6	100.0	12	6	BD181343	Method of
C 44	6	100.0	12	6	BD181357	Method of
C 45	6	100.0	12	6	BD184693	Method of

ALIGNMENTS

RESULT 1
CQ801400
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

CQ801400
Sequence 13 from Patent WO2004032958.
CQ801400
CQ801400.1 GI:47058061
unidentified
unclassified.
1
Pizza, M.C.
Polypeptide-vaccines for broad protection against hypervirulent
meningococcal lineages
Patent: WO 2004032958-A 13 22-APR-2004;
Chiron SRL (IT)
Location/Qualifiers
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/db_xref="taxon:32644"
/note="CpG motif"

linear PAT 05-MAY-2004

ORIGIN

Query Match
Best Local Similarity 100.0%; Score 6; DB 6; Length 6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GTCGTT 6
Db 1 GTCGTT 6

RESULT 2
AX104952
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AX104952
Sequence 1144 from Patent WO0122972.
AX104952
AX104952.1 GI:13921149
synthetic construct
synthetic construct

linear PAT 30-APR-2001

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 21, 2004, 05:50:35 ; Search time 70.1887 Seconds
(without alignments)
448.741 Million cell updates/sec

Title: US-09-337-584-57

Perfect score: 6

Sequence: 1 gtcgtt 6

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq 23Sep04:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	6	100.0	6	12	ADO04784
4	6	100.0	7	6	ABK46414
5	6	100.0	7	6	ABK46414
6	6	100.0	7	12	ADO04829
7	6	100.0	9	2	AAV09830
8	6	100.0	9	12	ADI16090
9	6	100.0	10	2	AAV50085
10	6	100.0	10	2	AAV35921
11	6	100.0	10	2	AAH86236
12	6	100.0	10	3	AAZ79656
13	6	100.0	10	3	AAZ83589
14	6	100.0	10	3	AAZ85678
15	6	100.0	10	3	AAZ85678
16	6	100.0	10	3	AAZ82614
17	6	100.0	10	3	AAZ84478
18	6	100.0	10	3	AAAL14249
19	6	100.0	10	3	AAZ93699
20	6	100.0	10	4	AAH64127
21	6	100.0	10	5	AAAF34602
22	6	100.0	10	5	AAAF38737

22	6	100.0	10	5	AAAF33302
23	6	100.0	10	5	AAAF34917
24	6	100.0	10	5	AAAF41756
25	6	100.0	10	5	AAAF36947
26	6	100.0	10	5	AAAF38736
27	6	100.0	10	5	AAAF36902
28	6	100.0	10	5	AAAF33387
29	6	100.0	10	5	AAAF34137
30	6	100.0	10	5	AAAF38738
31	6	100.0	10	5	AAAF39877
32	6	100.0	10	5	AAAF34209
33	6	100.0	10	5	AAAF36161
34	6	100.0	10	5	AAAF35922
35	6	100.0	10	5	AAAF39707
36	6	100.0	10	5	AAAF35436
37	6	100.0	10	5	AAAF43358
38	6	100.0	10	5	AAAF36915
39	6	100.0	10	5	AAAF38511
40	6	100.0	10	5	AAAF41520
41	6	100.0	10	5	AAAF37912
42	6	100.0	10	5	AAAF43262
43	6	100.0	10	6	ABK11499
44	6	100.0	10	6	ABK96563
45	6	100.0	10	9	ABZ81259

ALIGNMENTS

RESULT 1

ABK46412

ID ABK46412 standard; DNA; 6 BP.

XX AC ABK46412;

XX DT 05-JUN-2002 (first entry)

XX DE Immunostimulatory unmethylated CpG oligodeoxynucleotide #2.

XX KW unmethylated CpG; oligodeoxynucleotide; ON; virucide; vaccine;

XX KW Paramyxoviridae; F protein; respiratory syncytial virus; RSV;

XX KW viral bronchiolitis; pneumonia; infectious pulmonary disease;

XX KW bronchopulmonary dysplasia; congenital heart condition; ss.

XX OS Synthetic.

XX PN WO200211761-A2.

XX PD 14-FEB-2002.

XX PF 09-AUG-2001; 2001WO-US041633.

XX PR 10-AUG-2000; 2000US-0224011P.

XX PR 01-SEP-2000; 2000US-0229307P.

XX PA (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.

XX PI Mond JJ, Prince G, Kliman DM;

XX DR WPI; 2002-227119/28.

XX PT Vaccine for immunizing patient against respiratory syncytial virus, has

XX PT epitopes of Paramyxoviridae F protein, and cytosine followed by guanine

XX PT linked by phosphate bond-oligodeoxynucleotides.

XX XX Claim 4; Page 7; 30pp; English.

XX CC The invention describes a vaccine comprising one or more epitopes of a

XX CC Paramyxoviridae F protein, and one or more CpG (cytosine followed by

XX CC guanine linked by phosphate bond)-oligodeoxynucleotides (ODNs). The

XX CC vaccine is useful for vaccinating a patient especially against viruses of

XX CC the Paramyxoviridae family e.g. respiratory syncytial virus (RSV), the

XX CC primary cause of viral bronchiolitis and pneumonia in infants and

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OM nucleic - nucleic search, using sw model

Run on: December 21, 2004, 08:31:21 ; Search time 13.4717 Seconds
(without alignments)
316.570 Million cell updates/sec

Title: US-09-337-584-57

Perfect score: 6

Sequence: 1 gtcgtt 6

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

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- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	6	100.0	6	4	US-09-325-193A-95
4	6	100.0	6	4	US-09-347-343-24
5	6	100.0	6	4	US-09-337-619-57
6	6	100.0	7	3	US-09-030-701-17
7	6	100.0	7	4	US-09-325-193A-97
8	6	100.0	7	4	US-09-337-619-102
9	6	100.0	8	1	US-07-949-541A-9
10	6	100.0	8	1	US-07-949-541A-9
11	6	100.0	8	1	US-07-949-541A-14
12	6	100.0	8	3	US-09-527-234A-2
13	6	100.0	8	3	US-09-527-234A-2
14	6	100.0	8	4	US-09-527-233B-2
15	6	100.0	10	4	US-09-154-750A-39
16	6	100.0	10	4	US-09-508-753B-422
17	6	100.0	10	4	US-09-508-753B-422
18	6	100.0	12	1	US-08-053-131-8
19	6	100.0	12	1	US-08-645-641-8
20	6	100.0	12	1	US-07-853-408B-8
21	6	100.0	12	1	US-08-096-762-8
22	6	100.0	12	2	US-08-308-865-8
23	6	100.0	12	2	US-08-613-965-6
24	6	100.0	12	2	US-08-918-966-6
25	6	100.0	12	3	US-09-921-655-6
26	6	100.0	12	3	US-09-042-353-160
27	6	100.0	12	3	US-09-281-418-31

C 28	6	100.0	12	3	US-08-758-417A-8	Sequence 8, Appli
C 29	6	100.0	12	5	PCT-US92-10983-8	Sequence 8, Appli
C 30	6	100.0	13	3	US-09-336-228B-9	Sequence 9, Appli
C 31	6	100.0	13	3	US-09-030-701-56	Sequence 56, Appli
C 32	6	100.0	13	3	US-09-286-098-98	Sequence 98, Appli
C 33	6	100.0	13	3	US-08-960-774-85	Sequence 85, Appli
C 34	6	100.0	13	4	US-09-325-193A-84	Sequence 84, Appli
C 35	6	100.0	13	4	US-09-191-170-92	Sequence 92, Appli
C 36	6	100.0	13	4	US-08-862-629B-6	Sequence 6, Appli
C 37	6	100.0	13	4	US-08-862-629B-7	Sequence 7, Appli
C 38	6	100.0	13	4	US-08-862-629B-8	Sequence 8, Appli
C 39	6	100.0	13	4	US-09-083-235A-6	Sequence 6, Appli
C 40	6	100.0	13	4	US-09-083-235A-7	Sequence 7, Appli
C 41	6	100.0	13	4	US-09-083-235A-8	Sequence 8, Appli
C 42	6	100.0	13	4	US-09-337-619-85	Sequence 85, Appli
C 43	6	100.0	14	1	US-08-366-783-10	Sequence 10, Appli
C 44	6	100.0	14	3	US-08-834-765A-5	Sequence 5, Appli
C 45	6	100.0	14	3	US-09-078-283A-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-09-030-701-49
; Sequence 49, Application US/09030701B
; Patent No. 6214806
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schwartz, David A.
; TITLE OF INVENTION: USE OF NUCLEIC ACIDS CONTAINING
; TITLE OF INVENTION: UNMETHYLATED CPG DINUCLEOTIDE IN THE TREATMENT OF
; FILE REFERENCE: C1039/7011
; CURRENT APPLICATION NUMBER: US/09/030,701B
; CURRENT FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/039,405
; PRIOR FILING DATE: 1997-02-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 49
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-09-030-701-49

Query Match 100.0%; Score 6; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.1e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCGTT 6
Db 1 GTCGTT 6

RESULT 2

US-08-960-774-57
; Sequence 57, Application US/08960774
; Patent No. 6239116
; GENERAL INFORMATION:
; APPLICANT: Krieg et al.,
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID MOLECULES
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESS: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:

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OM nucleic - nucleic search, using sw model

Run on: December 21, 2004, 13:14:11 ; Search time 60.9057 Seconds
(without alignments)
543.874 Million cell updates/sec

Title: US-09-337-584-57

Perfect score: 6

Sequence: 1 gtcgtt 6

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4093002 seqs, 2760418825 residues

Total number of hits satisfying chosen parameters: 8186004

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:

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2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:
9: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:
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14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:
16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:
17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:
18: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:
19: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:
20: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:
21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	6	100.0	6	10	US-09-954-987B-66
2	6	100.0	6	13	US-10-023-909A-95
3	6	100.0	6	14	US-10-300-247-95
4	6	100.0	6	15	US-10-253-117-24
5	6	100.0	6	15	US-10-187-264A-57
6	6	100.0	6	15	US-10-306-522-57
7	6	100.0	6	15	US-10-314-578-1144
8	6	100.0	6	15	US-10-434-696-95
9	6	100.0	6	16	US-10-719-493-57
10	6	100.0	6	17	US-10-627-331-57
11	6	100.0	6	18	US-10-757-345-49
12	6	100.0	6	18	US-10-757-345-167

13	6	100.0	7	10	US-09-954-987B-120	Sequence 120, Appl
14	6	100.0	7	13	US-10-023-909A-97	Sequence 97, Appl
15	6	100.0	7	14	US-10-300-247-97	Sequence 97, Appl
16	6	100.0	7	15	US-10-187-264A-102	Sequence 102, Appl
17	6	100.0	7	15	US-10-306-522-102	Sequence 102, Appl
18	6	100.0	7	15	US-10-434-696-97	Sequence 97, Appl
19	6	100.0	7	16	US-10-719-493-102	Sequence 102, Appl
20	6	100.0	7	17	US-10-627-331-102	Sequence 102, Appl
21	6	100.0	7	18	US-10-757-345-48	Sequence 48, Appl
22	6	100.0	8	13	US-10-034-075-22	Sequence 2, Appl
23	6	100.0	8	15	US-10-314-578-1145	Sequence 1145, Ap
24	6	100.0	8	18	US-10-757-345-47	Sequence 47, Appl
25	6	100.0	9	18	US-10-613-524-4	Sequence 4, Appl
26	6	100.0	10	9	US-09-154-750A-39	Sequence 39, Appl
27	6	100.0	10	13	US-10-033-145-2084	Sequence 2084, Ap
28	6	100.0	10	15	US-10-330-627-967	Sequence 967, Appl
29	6	100.0	10	18	US-10-613-524-26	Sequence 26, Appl
30	6	100.0	10	18	US-10-816-220-429	Sequence 429, Appl
31	6	100.0	11	16	US-10-279-684A-33	Sequence 33, Appl
32	6	100.0	11	18	US-10-613-524-25	Sequence 25, Appl
33	6	100.0	11	18	US-10-757-345-26	Sequence 26, Appl
34	6	100.0	11	18	US-10-757-345-46	Sequence 46, Appl
35	6	100.0	11	18	US-10-757-345-159	Sequence 159, Appl
36	6	100.0	12	9	US-09-877-526A-36	Sequence 36, Appl
37	6	100.0	12	9	US-09-877-526A-38	Sequence 38, Appl
38	6	100.0	12	10	US-09-992-160-38	Sequence 38, Appl
39	6	100.0	12	10	US-09-992-160-38	Sequence 38, Appl
40	6	100.0	12	14	US-10-056-761-36	Sequence 36, Appl
41	6	100.0	12	14	US-10-056-761-38	Sequence 38, Appl
42	6	100.0	12	15	US-10-217-106-99	Sequence 99, Appl
43	6	100.0	12	15	US-10-217-106-100	Sequence 100, Appl
44	6	100.0	12	15	US-10-237-016-91	Sequence 91, Appl
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ALIGNMENTS

RESULT 1

US-09-954-987B-66
; Sequence 66, Application US/09954987B
; Publication No. US20030104523A1
; GENERAL INFORMATION:
; APPLICANT: Stefan Bauer
; APPLICANT: Grayson B. Lipford
; APPLICANT: Hermann Wagner
; TITLE OF INVENTION: PROCESS FOR HIGH THROUGHPUT SCREENING OF
; FILE REFERENCE: C1041/7016 (AWS)
; CURRENT APPLICATION NUMBER: US/09/954,987B
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: US 60/233,035
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/263,657
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: US 60/291,726
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: US 60/300,210
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 230
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 66
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-09-954-987B-66

Query Match 100.0%; Score 6; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 9e+08;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OM nucleic - nucleic search, using sw model

Run on: December 21, 2004, 08:28:35 ; Search time 796.019 Seconds
(without alignments)
274.665 Million cell updates/sec

Title: US-09-337-584-57

Perfect score: 6

Sequence: 1 gtcgtt 6

Scoring table: IDENTITY_NUC

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Searched: 32822875 seqs, 18219865908 residues

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 4	6	100.0	19	4	BM401163 5009-0-83
C 5	6	100.0	19	8	AZ595242 1M0407C15
C 6	6	100.0	19	8	AZ595242 1M0407C15
C 7	6	100.0	20	9	AZ954781 2M0220C07
C 8	6	100.0	21	4	BM398235 Arabidops
C 9	6	100.0	22	1	AA921198 5009-0-42
C 10	6	100.0	22	1	AA921198 5009-0-42
C 11	6	100.0	23	1	AI088271 5009-0-81
C 12	6	100.0	23	1	AJ790638 5009-0-81
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C 16	6	100.0	24	4	BM400996 Arabidops
C 17	6	100.0	24	6	BM401014 5009-0-81
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C 19	6	100.0	24	6	CF339742 RCL1--05-
C 20	6	100.0	24	8	AZ374821 1M0127G19
C 21	6	100.0	24	8	AZ474821 1M0292A16
C 22	6	100.0	24	8	BH857694 Arabidops
C 23	6	100.0	25	9	TA201F10P Arabidops
C 24	6	100.0	25	1	AI000280 Arabidops
C 25	6	100.0	25	1	AI638719 Arabidops

C 25	6	100.0	25	8	BH906076
C 26	6	100.0	25	8	BZ383367
C 27	6	100.0	25	8	CC455475
C 28	6	100.0	25	9	CG708827
C 29	6	100.0	26	6	CA587202
C 30	6	100.0	26	8	BH789316
C 31	6	100.0	26	8	BH909213
C 32	6	100.0	27	5	BX555323
C 33	6	100.0	27	5	BX555323
C 34	6	100.0	27	9	TA111H06Q
C 35	6	100.0	27	9	TA274G11P
C 36	6	100.0	27	9	AG187895
C 37	6	100.0	27	9	AG198308
C 38	6	100.0	28	1	AI641251
C 39	6	100.0	28	1	AI794924
C 40	6	100.0	28	5	BX555317
C 41	6	100.0	28	6	CF340587
C 42	6	100.0	28	8	AZ863855
C 43	6	100.0	28	9	AJ590490
C 44	6	100.0	29	6	CF281394
C 45	6	100.0	29	8	AQ025665

ALIGNMENTS

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LOCUS
DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

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